

GenCore version 5.1.4-p5-4578
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OM nucleic - nucleic search, using sw model

Run On: March 11, 2003, 15:26:24 ; Search time 1159 seconds

(without alignments)
8964.367 Million cell updates/sec

Title: US-09-936-011-1

Perfect score: 357
Sequence: 1 atgtctagggaataaccgc.....gtaatgtgtctgtgttaa 357

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba: *
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3: gb_in: *
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29: em_vl: *
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31: em_htg_inv: *
32: em_htg_other: *
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39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	357	6 AX039058	AX039058 Sequence
2	357	100.0	4612	14 TOBNVMP2	X04197 Beet necrot
3	355.4	99.6	1922	14 BNYVMP1	X75575 Beet necrot
4	347.4	97.3	357	6 AX039060	AX039060 Sequence
5	337.8	94.6	739	6 E59890	E59890 Rhizomania-
6	337.8	94.6	4544	14 AP197556	AP197556 Beet necr
7	337.8	94.6	4609	6 E59889	E59889 Rhizomania-
8	337.8	94.6	4609	14 BNYKPRO2	D84411 Beet necrot
9	333	93.3	4544	14 AP197547	AP197547 Beet necr
10	331.4	92.8	1922	14 BNYVMP2	X75574 Beet necrot
11	325	91.0	739	6 E59891	E59891 Rhizomania-
12	217.8	61.0	4616	14 AP061869	AP061869 Beet soil
13	68.6	19.2	3065	14 LRVBABC	Z45351 Lycinis rin
14	62.8	17.6	3005	14 BSBVJGNS	Z66493 Beet soil-b
15	57.8	16.2	3591	14 PSZBPTACD	M81486 Poa semilat
16	55.2	15.5	2529	14 BVO233598	AJ223598 Beet viru
17	51	14.3	3215	14 BSU35769	U35769 Barley strl
18	51	14.3	3237	14 BSU35772	U35772 Barley strl
19	51	14.3	3289	14 HOBMSVRB	X03854 Barley strl
20	50.8	14.2	4290	14 AF239729	AF239729 Indlqn pe
21	50.6	14.2	2962	14 PMXTGBP	D30753 Potato mop-
22	50.6	14.2	2964	14 PMO277556	AJ277556 Potato mo
23	50.6	14.2	4504	14 PMWRNATI	L07269 Peanut clum
24	50.2	14.1	2417	14 D86638	D86638 Broad bean
25	49.4	13.8	3239	14 BSU35770	U35770 Barley strl
26	49.4	13.8	3249	14 BSU35771	U35771 Barley strl
27	43	12.0	175495	2 AC023338	AC023338 Mus muscu
28	43	12.0	178870	2 AC021555	AC021555 Homo sapi
29	43	12.0	215738	2 AC113274	AC113274 Mus muscu
30	43	12.0	258120	2 AC114408	AC114408 Mus muscu
31	42.8	12.0	2325	14 NVMV2	D00906 Nicotiana v
32	42.4	11.9	204615	2 AC112254	AC112254 Homo sapi
33	41	11.5	171438	2 AC009231	AC009231 Rattus no
34	41	11.5	172076	2 AC121895	AC121895 Mus muscu
35	40	11.2	32070	2 AC116983	AC116983 Dictyoste
36	39	10.9	101149	2 AC118492	AC118492 Rattus no
37	38.8	10.9	205793	2 AC103615	AC103615 Mus muscu
38	38.4	10.8	171031	2 AC104020	AC104020 Homo sapi
39	38.2	10.7	16241	9 AC018713	AC018713 Homo sapi
40	38.2	10.7	205380	2 AC037488	AC037488 Homo sapi
41	37.8	10.6	133501	2 AC116956	AC116956 Dictyoste
42	37.8	10.6	179846	2 AC119387	AC119387 Rattus no
43	37.8	10.6	194158	2 AC107761	AC107761 Mus muscu
44	37.4	10.5	180214	2 AC101751	AC101751 Mus muscu
45	37.2	10.4	128433	2 AC124151	AC124151 Oryza sat

ALIGNMENTS

RESULT 1
AX039058
LOCUS
DEFINITION
Sequence 1 from Patent EP1038961.
AX039058
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 357)
AUTHORS
Lauber, E., Jonard, G., Guillely, H. and Richards, K.
TITLE
Method for inducing viral resistance into a plant
JOURNAL
Patent: EP 1038961-A 1 27-SEP-2000;
DE CENTRE NAT (FR)

Pred. No. is the number of results predicted by chance to have a

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FEATURES
    source          Location/Qualifiers
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                    /db_xref="taxon:31721"
                    1..357
                    /note="unnamed protein product"
CDS
    1..357
    /codon_start=1
    /protein_id="CA16570.1"
    /db_xref="GI:11228355"
    /translation="MSREITTPAPKKNVPIVGVVAFVLLAFMOOKKHTHSGDYG
    VPFTSNGIYRDGTRSDAFNSNNHRAVCGSGSVSRVGOOLIVLAIIVSLVLSLL
    ORLRSPPEHICNACG"
BASE COUNT      89 a      58 c      93 g      117 t
ORIGIN
Query Match      100.0%; Score 357; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-93;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATACCGCTGCACCCCAATAGATGCTATGTTGTTGTTGTTGT
    |||||||
    1 ATGCTAGGGAATACCGCTGCACCCCAATAGATGCTATGTTGTTGTTGTTGT
    |||||||
    61 GTTGTGGCTTCTTGTATTTGCTGGGCTCATGACAGCAAAACATAGACATTTGGG
    |||||||
    61 GTTGTGGCTTCTTGTATTTGCTGGGCTCATGACAGCAAAACATAGACATTTGGG
    |||||||
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    121 GGTGATTACGAGTCCCAACATTTTCTACAGCGTGATATATAGACGCTACAGATCA
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    QY 241 AGTAGTCAGTGGGACAGCACTTATTTGTTAGCTATTGTTCTGTGTTAATAGTCA
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    Db 241 AGTAGTCAGTGGGACAGCACTTATTTGTTAGCTATTGTTCTGTGTTAATAGTCA
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    QY 301 CTATTACACAGTATTAAGTCTCCACAGAACATTTGTAATGCTGCTGCTTAA
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    Db 301 CTATTACACAGTATTAAGTCTCCACAGAACATTTGTAATGCTGCTGCTTAA
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RESULT 2
LOCUS TOBNYV2 4612 bp RNA linear VRL 25-MAY-1999
DEFINITION Beet necrotic yellow vein virus RNA-2.
ACCESSION X04197
VERSION X04197.1 GI:62050
KEYWORDS coat protein; subgenome; unidentified reading frame.
SOURCE Beet necrotic yellow vein virus.
ORGANISM Beet necrotic yellow vein virus.
REFERENCE 1 (bases 1 to 4612)
AUTHORS Bouzoubaa,S., Ziegler,V., Beck,D., Guillely,H., Richards,K. and
Jonard,G.
TITLE Nucleotide sequence of Beet Necrotic Yellow Vein Virus RNA-2
JOURNAL J. Gen. Virol. 67, 1689-1700 (1986)
COMMENT Partial readthrough of the termination codon at position 709-711
gives rise to 75k protein
Data kindly reviewed (02-SEP-1987) by Bouzoubaa S.
FEATURES
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                    /organism="Beet necrotic yellow vein virus"
                    /strain="isolate P13"
                    /db_xref="taxon:31721"
                    /clone="pBp14, pBC2"
                    1..8
                    /note="Inverted repeat A"
                    repeat_unit 27..34
                    repeat_unit 145..2220
                    /note="Inverted repeat A"
                    CDS
                    145..2220
                    /note="75k protein (aa 1-691); read-through stop-codon"
                    /codon_start=1
                    /transl_except=(pos:709..711,aa:OTHER)
                    /protein_id="CA16351.1"
                    /db_xref="GI:4894189"
                    /translation="MSSEGRYMTWKDKSHKFMTRDRAVSDVSVIKOSHAMDLSKA
                    ANLSITKTLAAGSGSDSNPVSPTPTPQTITMAGALVLYNLSPERALTITKV
                    NLTLDGSLADNASANVRDVSNGNKAESSKRTAGTNSASATYTLISLAGLQALRLKE
                    LMTWDRKPEDREKLPMTPVQGRTPSPGOXOLAARVNAHIAAKRALLYPGDSPEWVK
                    WKHFYPPEDYDVPPLDIINAKLAADDIGGLVTPTPASSHGLPFVEYSEVEQANRN
                    SMLTVGLLLAALAIIGYVAHRRKASRLRELKILMGSTGGSGGGGFGELHTTRA
                    IDTVSLGTLSEHVAAPSGLRHRRPAATDSGPHVLPFEVWEPNNIAVYVSGISDIL
                    FYTREFVGFNGEEFGLLELSDPDDGVYTNAPDRLAIDATESQENTRIDVETV
                    LIERINIKKLLEAELELEREDMTIADEOELRLRLLESSVEATHTYTKADA
                    RAAVMAALASKEDANDYSKMAFDRCSEOLERLRLLELVNSPKEKTEHYVTLQIGA
                    OLAGAAVAGAMLRRGASSSSONSGANIGSRISOLIRGRASOPLRGSGSTRVNN
                    NLSNTNLYRAGNSAAVSACRSTNSGNSNWSKRLRVEGMSKYSVERAATPAORAIIV
                    PAPSAPAG"
                    145..711
                    /note="coat protein; 21k (aa 1-188)"
                    /codon_start=1
                    /protein_id="CA27791.1"
                    /db_xref="GI:62051"
                    /translation="MSSEGRYMTWKDKSHKFMTRDRAVSDVSVIKOSHAMDLSKA
                    ANLSITKTLAAGSGSDSNPVSPTPTPQTITMAGALVLYNLSPERALTITKV
                    NLTLDGSLADNASANVRDVSNGNKAESSKRTAGTNSASATYTLISLAGLQALRLKE
                    LMTWDRKPEDREKLPMTPVQGRTPSPGO"
                    <712..2220
                    /note="pot. 54k protein (aa 1-503)"
                    /codon_start=1
                    /protein_id="CA27792.1"
                    /db_xref="GI:1334951"
                    /translation="OLAARVTAHIAAKRALLYPGDSPEWVKHFFPPPYDYDV
                    PDLITNAKIADDIGVLYPTPAHRRKALLYPGDSPEWVKHFFPPPYDYDV
                    GGVAVYHRRKDSRLRELKILMGSTGGSGGGGFGELHTRAIDTVSLGTLSEHVA
                    PAPSGLRHRPAATDSGPHVLPFEVWFDNLAAVYDLSIGMSDLFTYREFVNGEEL
                    EGLIELLESDPDDGVYTNAPDRLAIDATESQENTRIDVETVLIERINIKKLLE
                    AELEREDMTIADEOELRLRLLESSVEATHTYTKADAARAAVMAALASKEDAN
                    DYDSKMAFDRCSEOLERLRLLELVNSPKEKTEHYVTLQIGAOLAGAAVAGAMLRRG
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                    /note="42k protein (aa 1-384)"
                    /codon_start=1
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                    /db_xref="GI:62053"
                    /translation="WVQVORRTGGDKCAKNRASSAPYRSRMTODDMSRTIPDDIFS
                    VIEKTLVEDDYKNGVYRGHCDWKLKESGAIIDNFRGTLEBELGRNCDLTCNAAVKL
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                    AGRLDFELVNDLFCRSVEYKNTMLADEVETRVHMCLEIIVLAGHGVNVCIFGDPAQ
                    GLNRYKASGNVANNPITIAECYASRRFKATIDLINSSGGGKPYVGNNEKSMFEE
                    LGCKIIDMSVIVLARETQKFLLEDNLSIISPAHQGVYVTVIILDEPDAIACD
                    PNRAVLLTRKNGKIMKGPNTIARRKNDGPNRSGVSKSGCTGDFCEDR"
                    3287..3643
                    /note="pot. 13k protein (aa 1-117)"
                    /codon_start=1
                    /protein_id="CA27794.1"
                    /db_xref="GI:62054"
                    /translation="MSREITTPAPKKNVPIVGVVAFVLLAFMOOKKHTHSGDYG
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                    ORLRSPPEHICNACG"
                    3627..4025
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                    /db_xref="GI:62055"
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CDS

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4043..4426

/note="pot. 14k protein (aa 1-127)"

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/protein_id="CAA27796.1"

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/translation="MGWVDSLGVFGRVITGESSEVEGERSEIKFSEMKLFTIAVY
EYRELGEKCSLKADGRILHFNYSVCKCOCKLCKKONKHNKSHVQNGYLRKVNPSIL
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polyA_site

4612

BASE COUNT 1200 a 760 c 1209 g 1443 t

ORIGIN

Query Match 100.0%; Score 357; DB 14; Length 4612;
Best Local Similarity 100.0%; Pred. NO. 1.6e-93;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS

QY 1 ATGCTAGGGAATAACCGCTCGACCAATAGAAATGTCCTATGTTGTTGTTGT 60
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DB 3287 ATGCTAGGGAATAACCGCTCGACCAATAGAAATGTCCTATGTTGTTGTTGT 3346
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QY 61 GTTGGGCTTTCTTTGATGCTGCGGTCATGCACAAAACATAAGACATCTGGG 120
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DB 3347 GTTGGGCTTTCTTTGATGCTGCGGTCATGCACAAAACATAAGACATCTGGG 3406
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QY 121 GGTGATTAAGAGTCCCAATTTCTAAGCGGTATATATAGACGGTACAGATCA 180
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DB 3407 GGTGATTAAGAGTCCCAATTTCTAAGCGGTATATATAGACGGTACAGATCA 3466
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QY 181 GCTGATTTTAAATAGTAACATCATCGCTTAACGGGTGGGTGCTGGGGTAGCGTT 240
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DB 3467 GCTGATTTTAAATAGTAACATCATCGCTTAACGGGTGGGTGCTGGGGTAGCGTT 3526
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QY 241 AGTACGCGTGGGAGCACTAATGTTAGTACGATATGTTCTGTGTAATAGTCA 300
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DB 3527 AGTACGCGTGGGAGCACTAATGTTAGTACGATATGTTCTGTGTAATAGTCA 3586
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QY 301 CTATTACAACGATTAAGTCTCCACAGAACATTTGTAATGCTGTTGGTTAA 357
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DB 3587 CTATTACAACGATTAAGTCTCCACAGAACATTTGTAATGCTGTTGGTTAA 3643
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RESULT 3

BNYVMTPL

LOCUS

DEFINITION

1922 bp RNA linear VRL 01-JUN-1994

transp. proteins.

VERSION

X75575.1 GI:496548

KEYWORDS

13k transport protein; 15k transport protein; 42k transport protein; transp. protein.

SOURCE

Beet necrotic yellow vein virus.

ORGANISM

viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.

REFERENCE

1 (bases 1 to 1922)

AUTHORS

Koenig, R.

JOURNAL

Unpublished (sites)

REMARK

2 (bases 1 to 1922)

TITLE

Solovayev, A.

FEATURES

location/Qualifiers

1..1922

/organism="Beet necrotic yellow vein virus"

/db_xref="taxon:31721"

1..1155

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CDS

CDS

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DTLQVKRTSSDMTARVGLVLPAGVKGSTSLNLDKFGAKRMYLCLPFSQLEBVF
AGRLDTELVLDLFCRSVEYGRYNTMLVDEVRVHNCETLLVLAGHGVKNVICFGDPAQ
GLNYKAGSAVNYNFPILAEYASRRFGATADLINSNGSGKPRVGNKNVKSMPFE
LCGKILDSSTVLVAATRETKFLIEDNITSILYSDAHGQYDVVTTIILEPDDAICD
PNVAVALTRARKGMIMGMRIARFRNGDPSNGVSKSTGIDFCEBR"

1155..1511

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/db_xref="SPTREMBL:Q65682"

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VPTNSNGKRYDRGSRADPNSNNHRAVCGSGSGSVSHVGOOLIVLAIVLSLL
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1495..1893

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/translation="MVLVKKYDLNIVLYIYVAGCVVNSLYSPFESNDVKASSYAGAI
FKSGCINDRNSFOFGCDIPKHVAESITVATKEHVDIVWKRGVTVRVVTLLET
IFILSRFLGLAVLFEMICLMSIWFVYHR"

BASE COUNT 505 a 309 c 506 g 602 t

ORIGIN

Query Match 99.6%; Score 355.4; DB 14; Length 1922;
Best Local Similarity 99.7%; Pred. NO. 4.4e-93;
Matches 356; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 GTTGGGCTTTCTTTGATGCTGCGGTCATGCACAAAACATAAGACATCTGGG 120
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DB 1275 GGTGATTAAGAGTCCCAATTTCTAAGCGGTATATATAGACGGTACAGATCA 1334
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QY 181 GCTGATTTTAAATAGTAACATCATCGCTTAACGGGTGGGTGCTGGGGTAGCGTT 240
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DB 1335 GCTGATTTTAAATAGTAACATCATCGCTTAACGGGTGGGTGCTGGGGTAGCGTT 1394
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QY 241 AGTACGCGTGGGAGCACTAATGTTAGTACGATATGTTCTGTGTAATAGTCA 300
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DB 1395 AGTACGCGTGGGAGCACTAATGTTAGTACGATATGTTCTGTGTAATAGTCA 1454
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QY 301 CTATTACAACGATTAAGTCTCCACAGAACATTTGTAATGCTGTTGGTTAA 357
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DB 1455 CTATTACAACGATTAAGTCTCCACAGAACATTTGTAATGCTGTTGGTTAA 1511
|||||

RESULT 4

AX039060

LOCUS

DEFINITION

357 bp DNA linear PAT 16-NOV-2000

AX039060

Sequence 3 from Patent EP1038961.

AX039060

AX039060.1 GI:11228356

KEYWORDS

Beet necrotic yellow vein virus.

ORGANISM

viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.

REFERENCE

1 (bases 1 to 357)

AUTHORS

Lauber, E., Jonard, G., Guille, H. and Richards, K.

TITLE

Method for inducing viral resistance into a plant

JOURNAL

Patent: EP 1038961-A 3 27-SEP-2000;
DE CENTRE NAT (FR)

FEATURES
Source Location/Qualifiers
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/organism="Beet necrotic yellow vein virus"
/db_xref="taxon:31721"
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/note="unnamed protein product"
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/db_xref="GI:11228357"
/translation="MSREITAPRNKNPVIVGCVVAFVLLAFMOAATHSGDYG
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ORLRSPEHICNACG"

BASE COUNT 84 a 60 c 96 g 117 t

ORIGIN

Query Match 97.3%; Score 347.4; DB 6; Length 357;
Best Local Similarity 98.3%; Pred. No. 8.7e-91;
Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 ATGCTAGGGAATTAACCGCTGACCAATTAAGATGCTTATGTTGGTGTTC 60
1 ATGCTAGGGAATTAACCGCTGACCAATTAAGATGCTTATGTTGGTGTTC 60

QY 61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGAAAACATTAAGACATTCGGG 120
61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120

Db 61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120
61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120

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121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGCGGTACAATCA 180

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QY 241 AGTAGTCAGTGGGACGACATTTATGTTGCTATGTTCTGTATATAGTGTCA 300
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Db 241 AGTAGTCAGTGGGACGACATTTATGTTGCTATGTTCTGTATATAGTGTCA 300
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QY 301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357
301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357

Db 301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357
301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357

RESULT 5
E59890 739 bp DNA linear PAT 31-JAN-2002
LOCUS Rhizomania-resisting plant.
DEFINITION E59890
ACCESSION E59890.1 GI:18622726
VERSION
KEYWORDS JP 20000312540-A/2.
SOURCE
ORGANISM
Beet necrotic yellow vein virus.
Beet necrotic yellow vein virus
viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
1 (bases 1 to 739)
AUTHORS Nomura,S., Kamitani,G., Saito,M., Kiguchi,T., Kusu,S. and Soma,C.
TITLE Rhizomania-resisting plant
JOURNAL Patent: JP 2000312540-A 2 14-NOV-2000;
GENICHI KAMITANI,SHADANHOJIN HOKKAIDO TENSAN KYOKAI
OS Beet Necrotic Yellow Vein Virus
PN JP 2000312540-A/2
PD 14-NOV-2000
PF 28-APR-1999 JP 1999122628
PR SHINJI NOMURA,GENICHI KAMITANI,MINAKO SAITO,TADAHIKO KIGUCHI,
PI SHUNZO KUSUME,
PI CHIHITO SOMA
PC A01H05/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC
FH key Location/Qualifiers
FT source 1..739
FT Location/Qualifiers
1..739

FEATURES
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BASE COUNT 184 a 114 c 189 g 252 t

ORIGIN

Query Match 94.6%; Score 337.8; DB 6; Length 739;
Best Local Similarity 96.6%; Pred. No. 5.9e-88;
Matches 345; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 1 ATGCTAGGGAATTAACCGCTGACCAATTAAGATGCTTATGTTGGTGTTC 60
1 ATGCTAGGGAATTAACCGCTGACCAATTAAGATGCTTATGTTGGTGTTC 60

QY 61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGAAAACATTAAGACATTCGGG 120
61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120

Db 61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120
61 GTTGCGCTTCTTTGATTTGCTGGCTTCATGACGACGACAGCATTCGGG 120

QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGCGGTACAATCA 180
121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGCGGTACAATCA 180

Db 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGCGGTACAATCA 180
121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGCGGTACAATCA 180

QY 181 GCTGATTTTAATAGTAACAATCATGCTGTACGGGTGGGTGGGTGAGCGTT 240
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Db 181 GCTGATTTTAATAGTAACAATCATGCTGTACGGGTGGGTGGGTGAGCGTT 240
181 GCTGATTTTAATAGTAACAATCATGCTGTACGGGTGGGTGGGTGAGCGTT 240

QY 241 AGTAGTCAGTGGGACGACATTTATGTTGCTATGTTCTGTATATAGTGTCA 300
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Db 241 AGTAGTCAGTGGGACGACATTTATGTTGCTATGTTCTGTATATAGTGTCA 300
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QY 301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357
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Db 301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357
301 CTATTACAACGATTAAAGTCTCCACGAGAACACATTTGTAATGGTCTGTGTAA 357

RESULT 6
AF197556 454 bp RNA linear VRL 04-DEC-2000
LOCUS Beet necrotic yellow vein virus isolate Kas3 RNA 2 segment, partial
DEFINITION AF197556
ACCESSION AF197556
VERSION AF197556.1 GI:11528045
KEYWORDS
KEYWORDS Beet necrotic yellow vein virus.
SOURCE Beet necrotic yellow vein virus
ORGANISM Beet necrotic yellow vein virus.
Beet necrotic yellow vein virus
viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
1 (bases 1 to 454)
AUTHORS Koenig,R. and Lemmefors,B.L.
TITLE Molecular analyses of European A, B and P type sources of Beet
JOURNAL necrotic yellow vein virus and detection of the rare P type in
Kazakhstan
Arch. Virol. 145 (8), 1561-1570 (2000)
MEDLINE 20456802
PUBMED 11003469
REFERENCE 2 (bases 1 to 454)
AUTHORS Koenig,R.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) Institut fuer Pflanzenvirologie,
Mikrobiologie und Biologische Sicherheit, Biologische Bundesanstalt
fuer Land und Forstwirtschaft, Messeweg 11, D 38104 Braunschweig D
38104, Germany
Location/Qualifiers
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/organism="Beet necrotic yellow vein virus"
/isolate="Kas3"
/db_xref="taxon:31721"
/country="Kazakhstan"
/note="closely related to P type
almost complete sequence of RNA 2; lacks only a few
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type: P; segment: RNA 2"
join(107..670,674..2179)
/note="contains read-through stop codon"
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LMTPTKEDRLKMPVQGRTPSPGOOLAAARVAHIAAKRALLYPDSEBVMGM
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LMLTVGLLALAVGIGVAHYRRKLOSRLRELKLMGSGSGGGGGGPTTLYMRAT
DIVSLGTTLSEHAASAPGLRHRPATDOSPHEALPEVWAPNLSVYDSIGMSDF
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AAVAMTALASKANDYDSKMAEDRSCDELRLELVMSMPSKTERVYVGTIOGQAO
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PSPAPAG"
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AGRLDTFLVDLFCRSVEGKNTMLVDEVTYHMEKILYLACHLKVNYTCGDPHO
CLNKAGSAVNTPPIAECTASRRKRTADLINSNGGKVVANNEKVTGDFE
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/db_xref="GI:11528048"
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movement"
/codon_start=1
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/db_xref="GI:11528049"
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4002..4385
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/db_xref="GI:11528050"
/translation="MGWVDSLCEVGRVITGESSEVEGERSIKRESEKLLTAYV
EYRQGEKESLKVGRGLHFNKMSYCKCRKLCEKONKNSHVNQNGYLRKVRNSIL
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BASE COUNT 1174 a 756 c 1207 g 1407 t
ORIGIN
Query Match 94.6%; Score 337.8; DB 14; Length 4544;
Best Local Similarity 96.6%; Pred. No. 6.5e-88;
Matches 345; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATAACCGCTGACCCCAATTAAGATGCTATTTGTTGTTGTTGT 60
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DB 3246 ATGCTAGGGAATAACCGCTGACCCCAATTAAGATGCTATTTGTTGTTGTTGT 3305
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QY 61 GTTGGGCTTTCTTTGTAATGCTGCTTACGACGAAACATTAAGACACTTCTGGG 120
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DB 3306 GTTGTGCTTTCTTTGTAATGCTGCGCTTCATGACGAAACATTAAGACACTTCTGGG 3365
QY 121 GGTGATTAACGAGTCCCAACATTTTCTTAACGCTGTGATATATAGACGCTTACAGATCA 180
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DB 3366 GCGGATTAACGAGTCCCAACATTTTCTTAACGCTGTGATATATAGACGCTTACAGATCA 3425
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QY 181 GGTGATTTTAATAGTAACATCATGCTGCTTACGGGTGCGGTGCTGGGGGAGCGGT 240
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DB 3426 GCTGATTTTAATAGTAATATATATATATATATATATATATATATATATATATATATAT 3485
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QY 241 AGTACGAGTTGGGACGACCACTTATTTGTTAGTATTTCTGTGTTAATAGTGTCA 300
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DB 3486 AGTATTCGAGTGGGACGACCACTTGTGTTAGTATTTCTGTGTTAATAGTGTCA 3545
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QY 301 CTATTACACAGTTTAAGCTCTCCACAGAACACTTTGTAATGCTGTGTGTAA 357
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DB 3546 GTTGTACACAGTTTAAGATCTCCACAGAACACTTTGTAATGCTGTGTGTAA 3602
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RESULT 7
E59889
LOCUS E59889 4609 bp DNA linear PAT 31-JAN-2002
DEFINITION Rhizomania-resisting plant.
ACCESSION E59889
VERSION E59889.1 GI:18622725
KEYWORDS JP 2000312540-A/1.
SOURCE
ORIGINISM
REFERENCE
1 (bases 1 to 4609)
AUTHORS Nomura,S., Kamitani,G., Saito,M., Kiguchi,T., Kusu,S. and Some,C.
TITLE Rhizomania-resisting plant
PATENT: JP 2000312540-A 1 14-NOV-2000;
JOURNAL GENICHI KAMITANI,SHADANHOJIN HOKKAIDO TENSAN KYOKAI
COMMENT
OS Beet necrotic yellow vein virus
PD JP 2000312540-A/1
PE 14-NOV-2000
PR 28-APR-1999 JP 1999122628
PI SHINJI NOMURA,GENICHI KAMITANI,MIMAKO SAITO,TADAHIKO KIGUCHI,
PI SHUNZO KUSOME,
PI CHIHITO SOMA
PC A01H5/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC
FH key location/Qualifiers
FT source 1..4609
FEATURES
location/Qualifiers
1..4609
/organism="Beet necrotic yellow vein virus"
BASE COUNT 1187 a 765 c 1221 g 1436 t
ORIGIN
Query Match 94.6%; Score 337.8; DB 6; Length 4609;
Best Local Similarity 96.6%; Pred. No. 6.5e-88;
Matches 345; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATAACCGCTGACCCCAATTAAGATGCTATTTGTTGTTGTTGT 60
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DB 3284 ATGCTAGGGAATAACCGCTGACCCCAATTAAGATGCTATTTGTTGTTGTTGT 3343
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QY 61 GTTGGGCTTTCTTTGTAATGCTGCTTACGACGAAACATTAAGACACTTCTGGG 120
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DB 3344 GTTGTGCTTTCTTTGTAATGCTGCTTACGACGAAACATTAAGACACTTCTGGG 3403
|||||
QY 121 GGTGATTAACGAGTCCCAACATTTTCTTAACGCTGTGATATATAGACGCTTACAGATCA 180
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DB 3404 GCGGATTAACGAGTCCCAACATTTTCTTAACGCTGTGATATATAGACGCTTACAGATCA 3463
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QY 181 GGTGATTTTAATAGTAACATCATGCTGCTTACGGGTGCGGTGCTGGGGGAGCGGT 240
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DB 3464 GCTGATTTTAATAGTAATATATATATATATATATATATATATATATATATATATAT 3523
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QY	241	AGTACTGCGCTGGCGACGACACTTATGTGTACTATGTTCTGCTGTTAATAGTCTA	300
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QY	301	CTATTACACGATTAAAGTCTCCACGACACATTTGTATATGTCCTTGCGTTAA	357
Db	3584	CTGTTACACGATTAAAGTCTCCACGACACATTTGTATATGTCCTTGCGTTAA	3640
RESULT 8			
BNYKPRO2			
LOCUS			
DEFINITION	BNYKPRO2	4609 bp RNA linear	VR1 06-FEB-1999
ACCESSION		Beet necrotic yellow vein virus genomic RNA for 42k protein, 13k protein, 15k protein, 14k protein, 75k protein.	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
REFERENCE			
AUTHORS			
TITLE			
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AUTHORS			
TITLE			

[illegible]

ACCESSION	AF197547	sequence.
VERSION	AF197547.1	GI:11528023
KEYWORDS		
SOURCE		Beet necrotic yellow vein virus.
ORGANISM		Beet necrotic yellow vein viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
REFERENCE		1 (bases 1 to 4544)
AUTHORS	Koenig R. and Lennemann B.L.	
TITLE	Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan	
JOURNAL	Arch. Virol. 145 (8), 1561-1570 (2000)	
MEDLINE	20456802	
PUBMED	11003469	
REFERENCES	2 (bases 1 to 4544)	
AUTHORS	Koenig R.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-OCT-1999) Institut fuer Pflanzenvirologie, Mikrobiologie und Biologische Sicherheit, Biologische Bundesanstalt fuer Land und Forestwirtschaft, Messeweg 11, D 38104 Braunschweig D 38104, Germany	
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CDS		3246..3602 /note="second triple gene block; necessary for virus movement"
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CDS		/codon_start=1 /product="unknown" /protein_id="AA637082.1" /db_xref="GI:11528027" /translation="MVLVVKYDLSINLYIYVAGCVVYSMLSPFNSDVKASSYAGAV FRGSGCIIIDRNRFQFCSCDIPKHVASITIKVATKEHDADVMMKRGEVTRYVPTET IFILSRFLGLAVFLPMICLMASYFMCHR" 4002..4385 /codon_start=1 /product="P14 protein" /protein_id="AA637083.1" /db_xref="GI:11528028" /translation="MGWVDSLQVFGVGVITEGSRVSGVRFSTKSEMKLFPTTAIV EYRGCKRESLKDVGCLHLNMKSMVCCKRLKCKONKNSKHVONGYLNKVRNSTL GVGDCCESTFLDEKHVIYDPEV"
CDS		
BASE COUNT	1174 a	766 c 1205 g 1399 t
ORIGIN		
Query Match	93.3%	Score 333; DB 14; Length 4544;
Best Local Similarity	95.8%	Pred. No. 1.7e-86;
Matches 342:	Conservative 0;	Mismatches 15; Indels 0; Gaps 0;
Oy 1	ATGCTAGGGAATTAACCGCTGCAGCCCAATAAGAATGCTATTGTTGCTGTTTGT 60	
Db 3246	ATGCTAGGGAATTAACCGCTGCAGCCCAATAAGAATGCTATTGTTGCTGTTTGT 3305	
Oy 61	GTTGCGCTTTCTTGTATGCTGCGCTCATGCAGCAAAAACATTAGCACATTCTGGC 120	
Db 3306	GTTGCGCTTTCTTGTATGCTGCGCTCATGCAGCAAAAACATTAGCACATTCTGGC 3365	
Oy 121	GGTAGTACGAGTCCCAACATTTTCTAACCGTGTATATAGACGATACAAGATCA 180	
Db 3366	GGTAGTACGAGTCCCAACATTTTCTAACCGTGTATATAGACGATACAAGATCA 3425	
Oy 181	GCTATTTTTAATAAATCATATCGTGTCTTACGGGTGCGGTGGTCTGGGCTAGCGCTT 240	
Db 3426	GCTATTTTTAATAAATCATATCGTGTCTTACGGGTGCGGTGGTCTGGGCTAGCGCTT 3485	
Oy 241	AGTAGTCAGATGGCGACAACTATTGTGTACTTATTTGTTGTTGTTAATGTGTCA 300	
Db 3486	AGTAGTCAGATGGCGACAACTATTGTGTACTTATTTGTTGTTGTTAATGTGTCA 3545	
Oy 301	CTATTACACGATTAAGGCTCCACACGACAACTTTGTATGCTGCTTGCTTAA 357	
Db 3546	CTATTACACGATTAAGGCTCCACACGACAACTTTGTATGCTGCTTGCTTAA 3602	
RESULT 10		
BENVMP2		
LOCUS	BENVMP2	1922 bp RNA linear VRL 01-AUG-1994
DEFINITION	Beet necrotic yellow vein mosaic virus (Yu2) genomic RNA for transport proteins.	
ACCESSION	X75574	
VERSION	X75574.1	GI:496552
KEYWORDS	13k transport protein; 15k transport protein; 42k transport protein; transport protein.	
SOURCE	Beet necrotic yellow vein virus.	
ORGANISM	Beet necrotic yellow vein virus.	
REFERENCE	1 (bases 1 to 1922)	
AUTHORS	Kruse M., Koenig R., Hoffmann A., Kaufmann A., Commandeur U., Solovjev A.G., Savenkov I. and Burghmeister W.	
TITLE	Restriction fragment length polymorphism analysis of reverse transcription-PCR products reveals the existence of two major strain groups of beet necrotic yellow vein virus	
JOURNAL	J. Gen. Virol. 75 (Pt 8), 1835-1842 (1994)	
MEDLINE	94321971	

PUBMED 7913953
 REFERENCE 2 (bases 1 to 1922)
 AUTHORS Solov'yev, A.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1993) Solov'yev A., Institute for Biochemistry and Plant Virology, Messweg 11/12, Braunschweig, Germany
 FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:31721"
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 AGRLDTFLVDLFCRSVERGKYNTMLVDEVTYHMCLELLVAGHLGKYNVICPDPAQ
 GLANKGSAVNVNPIITAEVCYARRRGRKATADLINSNGGKRVGVNENKEDSWTFEE
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 1155..1511
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 /db_xref="SPTREMBL:Q65685"
 /translation="AVLVKVDLSNIVLYIVAGCVVVSMLYSPFESNDVKASSYAGAV
 FKSGCIMDRNSFOFGSDIPKHVAESTTAKTKRHDADIMVKRGDVTYRVVLTLET
 IFILLSRFGIAVEFPMICLMSIYPMWRH"
 1915..2400
 BASE COUNT 505 a 309 c 509 g 599 t
 ORIGIN
 Query Match 92.8%; Score 331.4; DB 14; Length 1922;
 Best local similarity 95.5%; Pred. No. 4,6e-86;
 Matches 341; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ATGCTAGGGAATAACCGCTGACCCCAATAGATGCTATGTTGTTGTTGTTGT 60
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 DB 1155 ATGCTAGGGAATAACCGCTGACCCCAATAGATGCTATGTTGTTGTTGTTGT 1214
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 QY 61 GTTGGGCTTTCTTTGTATGCTGGGCTCATGACGAAAAACATAGACATCTCGG 120
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 DB 1215 GTTGGGCTTTCTTTGTATGCTGGGCTCATGACGAAAAACATAGACATCTCGG 1274
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 QY 121 GGTGATTCAGGAGTCCCAACATTTCTAACGGGTATATATAGAGACGGTACAGTCA 180
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 DB 1275 GGTGATTCAGGAGTCCCAACATTTCTAACGGGTATATATAGAGACGGTACAGTCA 1334
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 QY 181 GCTGATTTAATAGTAACAATCATGCTTACGGGTGCGGTGGGTGCGGTACCGTT 240
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 DB 1335 GCTGATTTAATAGTAACAATCATGCTTACGGGTGCGGTGGGTGCGGTACCGTT 1394
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 QY 241 AGTAGTCAGATTGGGACGACACTTATGCTAGCTATTTGTTCTGTGTTAATAGTGCA 300
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 DB 1395 AGTAGTCAGATTGGGACGACACTTATGCTAGCTATTTGTTCTGTGTTAATAGTATTA 1454
 |||||||
 QY 301 CTATTACAAGATTAGGCTCCACAGAACACATTTGTAATGGTGTGTTGTTAA 357
 |||||||
 DB 1455 CTGTTACAAGATTAGGCTCCACAGAACACATTTGTAATGGTGTGTTGTTAA 1511
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RESULT 11
 LOCUS E59891 739 bp DNA linear PAT 31-JAN-2002
 DEFINITION Rhizomania-resisting plant.
 ACCESSION E59891
 VERSION E59891.1 GI:18622727
 KEYWORDS JP 2000312540-A/3.
 SOURCE Beet necrotic yellow vein virus.
 ORGANISM Beet necrotic yellow vein virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 1 (bases 1 to 739)
 REFERENCE
 1. (bases 1 to 739)
 AUTHORS Nomura, S., Kamitani, G., Saito, M., Kiguchi, T., Kusu, S. and Soma, C.
 TITLE Rhizomania-resisting plant
 JOURNAL Patent: JP 2000312540-A/3 14-NOV-2000;
 GENICHI KAMITANI, SHADANHOJIN HOKKAIDO TENSAI KYOKAI
 OS Beet Necrotic Yellow Vein Virus
 PN JP 2000312540-A/3
 PD 14-NOV-2000
 PF 28-Apr-1999 JP 1999122628
 PR
 PI SHINJI NOMURA, GENICHI KAMITANI, MINAKO SAIJO, TADAHIKO KIGUCHI,
 PI SHUNZO KUSUME,
 PI CHIHIRO SOMA,
 PI A01H5/00, C12N5/09, C12N5/00, C12N15/00 CC
 PC
 PH Key
 FT mutation
 Location/Qualifiers
 1..739
 /organism="Beet necrotic yellow vein virus"
 /db_xref="taxon:31721"
 BASE COUNT 182 a 117 c 187 g 253 t
 ORIGIN
 Query Match 91.0%; Score 325; DB 6; Length 739;
 Best local similarity 94.4%; Pred. No. 3.3e-84;
 Matches 337; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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 QY 61 GTTGGGCTTTCTTTGTATGCTGGGCTCATGACGAAAAACATAGACATCTCGG 120
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 DB 61 GTTGGGCTTTCTTTGTATGCTGGGCTCATGACGAAAAACATAGACATCTCGG 120
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 DB 241 AGTAGTCAGATTGGGACGACACTTATGCTAGCTATTTGTTCTGTGTTAATAGTATTA 300
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 QY 301 CTATTACAAGATTAGGCTCCACAGAACACATTTGTAATGGTGTGTTGTTAA 357
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 DB 301 CTGTTACAAGATTAGGCTCCACAGAACACATTTGTAATGGTGTGTTGTTAA 357
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 RESULT 12
 LOCUS AF061869 4616 bp RNA linear VRL 26-MAR-2002
 DEFINITION Beet soil-borne mosaic virus RNA2, complete genome.
 ACCESSION AF061869
 VERSION AF061869.1 GI:3136264
 KEYWORDS
 SOURCE beet soil-borne mosaic virus.
 ORGANISM beet soil-borne mosaic virus
 Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 1 (bases 1 to 4616)

AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 USA

Lee, L., Telford, E. B., Batten, J. S., Scholtz, K. B. and Rush, C. M.
 Complete nucleotide sequence and genome organization of Beet
 solborne mosaic virus, a proposed member of the genus Benyvirus
 Arch. Virol. 146 (12), 2443-2453 (2001)
 21670014
 11811691
 2 (bases 1 to 4616)
 Batten, J. S., Rush, C. M. and Scholtz, K. B. G.
 Direct Submission
 Submitted (28-APR-1998) Plant Pathology and Microbiology, Texas A&M
 University, 120 Peterson Building, College Station, TX 77843-2132,
 USA

REMARK	REFERENCE	(sites)
AUTHORS	Solov'ev, A.	2 (bases 1 to 3065)
TITLE	Direct Submission	
JOURNAL	Submitted (21-OCT-1994) Solov'ev A., Institute of Biochemistry and Plant Virology, Messweg 11/12, Braunschweig, Germany	
FEATURES	Location/Qualifiers	
source	1..3065	
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QY	121	GGTATTACGAGCTCCACACATTTTCTAACGGTGGTATATATAGACGCGTACAGATCA	180
Db	2300	GATTAAT-----ATTCAACAATTTGCCAACGGTGGTCTTATCAAGACGATTAATAAGA	2353
QY	181	GCTGATTTTATATAGTACCAATCATCGTCTTACGGGT	217
Db	2354	ATAAATTATACAAAAATAAATAATTACCTTACGGTT	2390
RESULT 14			
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LOCUS	BSBV3GNS	3005 bp	RNA
DEFINITION	Beet soil-borne virus genes for 13K, 22K and 48K proteins.		linear
ACCESSION	266493		
VERSION	266493.2	GI:11595427	
KEYWORDS	13K protein; 22K protein; 48K protein.		
SOURCE	Beet soil-borne virus.		
ORGANISM	Beet soil-borne virus		
REFERENCE	1 (bases 1 to 3005)		
AUTHORS	Koenig, R., Beter, C., Commandeur, U., Luth, U., Kaufmann, A. and		
TITLE	Lueddecke, P.		
JOURNAL	Beet soil-borne virus RNA 3--a further example of the heterogeneity		
MEDLINE	of the gene content of furovirus genomes and of triple gene		
PUBMED	block-carrying RNAs		
REFERENCE	Virology 216 (1), 202-207 (1996)		
AUTHORS	96187804		
TITLE	8614988		
JOURNAL	2 (bases 1 to 3005)		
REFERENCE	Koenig, R.		
AUTHORS	Direct Submission		
TITLE	Submitted (20-OCT-1995) Koenig R., Biologische Bundesanstalt fuer		
JOURNAL	Land- und Forstwirtschaft, Institut fuer		
REFERENCE	Biochemie/Pflanzenvirologie, Messegew 11, Braunschweig, Germany,		
AUTHORS	D38104		
TITLE	Revised by [3]		
JOURNAL	3 (bases 1 to 3005)		
REFERENCE	Koenig, R.		
AUTHORS	Direct Submission		
TITLE	Submitted (04-DEC-2000) Koenig R., Biologische Bundesanstalt fuer		
JOURNAL	Land- und Forstwirtschaft, Institut fuer		
REFERENCE	Biochemie/Pflanzenvirologie, Messegew 11, Braunschweig, Germany,		
AUTHORS	D38104		
COMMENT	On Dec 6, 2000 this sequence version replaced gi:1225930.		
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source	Location/Qualifiers		
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	KHLRKRPPSFLAGSVTVGPSSKTELLRKIQTEGAGLNSVYLVANERARKIFETQPA		
	CTAKETILLRTAIKYDVLIDEVTLADNCGEILLIQRILIEAKVAVLFGDRAQGNSTRA		
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	2462.. 3005
BASE COUNT	917 a 507 c 664 g 917 t
ORIGIN	
3'UTR	
PBS	
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Best Local Similarity	60.1%; Pred. No. 1.7e-07;
Matches 125;	Conservative 0; Mismatches 77; Indels 6; Gaps 1;
OY.	5 CTAGGGAATAACCGCTGCACCATTAAAGAATGTGCCATTGTGTGGTGTTGTG 64
Dd	1685 CTAATGAGATCGCGCCCAAGACTTAATGAATGTGGCCAATAGTCTGGTGATTGGCA 1744
OY	65 TGGCTTTCTGTGATTTGCTGCGCTTCATGACGACAATAACATTAACACATTCGTGGGGTG 124
Dd-	1745 TTGCATTGTCTAGTTTTTAACATACTAATCATCAGAACACGCCACAGTCGGAGATA 1804
OY	125 ATTAGGAGATCCCAACATTTTCTAACGGTGTATATATAGAGACGTAACAAGATCAGCTG 184
Dd	1805 ATA-----TCACAGAATTTCTTAACGGTGGAAAAATTCAAGACGCAATAAGCGTGTTC 1858
OY	185 ATTTAATAGTAACAATCATCGTGGCTTA 212
Dd	1859 ATTATAATAGAAATATCTTAGAGCTTA 1886
RESULT 15	
PSZBETACD	3591 bp ss-RNA linear VRL_02-AUG-1996
LOCUS	Poa semilient virus beta genomic segment beta-A, beta-B, beta-C
DEFINITION	Poa semilient virus beta genomic segment complete cds.
ACCESSION	M81486
VERSION	M81486.1 GI:1478094
KEYWORDS	
SOURCE	Poa semilient virus cDNA to genomic RNA.
ORGANISM	Poa semilient virus
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage: Hordeivirus. 1 (bases 1 to 3591)
AUTHORS	Agranovsky,A.A., Karasev,A.V., Novikov,V.K., Lunina,N.A., Loghinov,S. and Tyulkina,L.G.
TITLE	Poliovirus-like virus, a hordevirus having no internal polydispense poly(A) in the 3' non-coding region of the RNA genome
JOURNAL	J. Gen. Virol. 73 (Pt 8), 2085-2092 (1992)
MEDLINE	92356087
PUBMED	1645144
REFERENCE	2 (bases 1 to 3591)

AUTHORS	Solovery,A.G., Sevenkov,E.I., Agrirovsky,A.A. and Morozov,S.Y.
TITLE	Comparisons of the genomic cis-elements and coding regions in RNA beta components of the hordeivirus barley stripe mosaic virus, lynchis ringspot virus, and poa semillatent virus
JOURNAL	Virology 219 (1), 9-18 (1996)
MEDLINE	96204567
PUBMED	8623558
REFERENCE	3 (bases 1 to 3591)
AUTHORS	Solovery,A.
TITLE	Direct Submision
JOURNAL	Submitted (13-AUG-1993) Andrej G. Soloverye, Institute of Biochemistry and Plant Virology, Braunschweig, D-38104, Germany On Aug 2, 1996 this sequence version replaced gl:333326.
COMMENT	location/Qualifiers
FEATURES	1..3591
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CDS	826..2256
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BASE COUNT	1049 a 718 c 842 g 982 t
ORIGIN	
Query Match	16.2% Score 57.8; DB 14; Length 3591;
Best Local Similarity	60.0%; Pred. No. 5.le-05;
Matches 117; Conservative	0; Mismatches 72; Indels 6; Gaps 1;
21 TCGACCAATAAGAATGCGCATATGTTGGTGCGGCTTGTGTTGGCGTTTCCTTGGATT 80	

Accession	Sequence	Position
Db	2568 TAGACCTAATAGTATTTGGCCAACTTGTACTGCTATAGGTGTAGTAGTATTATTGGCTA	2647
QY	81 GCTGGCGTTTCATGCACGCAAAACATATAGACACATCTTGGGGGTGATTACGGAGTCCCAAC	140
Db	2648 CTTATATTTTGGCTAATCAACAAACATCTCTACTGATCTGGGAGTAATAT-----TCCCAAA	2701
QY	141 ATTTCCTAAGCGGTGTATATATAGACGGTACAAAGTCAGTCGATTTTATATAGTACAA	200
Db	2702 ATTTTCCCAACGGGTGGAGTATTCGACAGCGTCTTAAGTGTATTTCTTACCATCGAAMACA	2761
QY	201 TCATGCTGCTTACGG 215	
Db	2762 CCCTTTCGGCTAATGG 2776	

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Job time : 1179 secs

GenCore version 5.1.4_p5-4578
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 14:24:19 ; Search time 175 Seconds
(without alignments)

4594.077 Million cell updates/sec

Title: US-09-936-011-1

Sequence: 1 acgtctagggaataacgcgc.....gtaatgctctgtgtta 357

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	357	21	AAA75877
2	347.4	97.3	357	21	AAA75878
3	337.8	94.6	739	22	AAAF26890
4	337.8	94.6	4609	22	AAAF26889
5	325	91.0	739	22	AAAF26891
6	53.8	15.1	507	24	ABK86954
7	45.8	12.8	507	24	ABK86955
8	36.6	10.3	4039	22	AAH34822
9	36.6	10.3	4039	24	ABL90346

10	36.6	10.3	4040	21	AACT7977	Human cancer assoc
11	36.6	10.3	554	24	ABL61761	Colon adenocarcinoma
12	36.6	10.3	554	23	AA587055	DNA encoding novel
13	35.6	10.0	1668	24	ABK40083	Human chemically p
14	35.6	10.0	6725	24	ABL33209	Human immune syste
15	35.6	10.0	6725	24	ABL34555	Human metacarcinoma
16	35.2	9.9	3001	21	AAH51765	Chromosome 13q11-q
17	35	9.8	759	19	AAV28675	Ripening banana pu
18	34.6	9.7	2772	23	ABL25868	Drosophila melanog
19	34.4	9.6	1143	23	AA577359	DNA encoding novel
20	34.4	9.6	2263	23	AA588931	DNA encoding novel
21	34.2	9.6	2328	24	AA584696	Signal transductio
22	34.2	9.6	2494	24	ABK31539	Human immune/haema
23	34.2	9.6	5296	22	AAK77661	Human chemically t
24	34	9.5	7434	24	AAK28386	Human ORE840 cDNA
25	33.8	9.5	406	24	ABN75893	Human immune syste
26	33.8	9.5	6531	24	ABL32640	Human growth facto
27	33.6	9.4	1110	21	AAK81556	Yeast AOD9604-asso
28	33.6	9.4	4590	22	AAH24065	Arabidopsis thalia
29	33.2	9.3	1683	21	AAK37459	Human immune syste
30	33.2	9.3	5971	24	ABL32383	Tumour suppressor
31	33	9.2	14147	22	AA546743	Human DNA for stag
32	33	9.2	14147	24	ABK33955	Human immune syste
33	32.8	9.2	6535	24	ABL2937	Human gene regulat
34	32.6	9.1	5986	24	AA561433	Signal transductio
35	32.6	9.1	5986	24	ABK31439	Human prostate exp
36	32.4	9.1	487	23	ABV51629	Chitinase 1 gene.
37	32.4	9.1	2527	15	AAO56756	Human ovarian canc
38	32.4	9.1	2585	24	ABL87903	DNA encoding novel
39	32.4	9.1	3297	23	AA591437	Drosophila melanog
40	32.4	9.1	29376	23	ABL08834	Human foetal liver
41	32.2	9.0	234	22	ABA71836	Human brain expre
42	32.2	9.0	234	22	AAK20212	Human bone marrow
43	32.2	9.0	234	22	AAK46281	Probe #20866 used
44	32.2	9.0	234	22	AA52180	Human genome-deriv
45	32.2	9.0	234	24	AB520595	

ALIGNMENTS

RESULT 1	
AAA75877	
ID	AAA75877 standard; DNA; 357 BP.
XX	
AC	AAA75877;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	DNA encoding a P13 protein of Beet necrotic yellow vein mosaic virus.
XX	
KW	P13 protein; triple gene block 2; TGB2; resistance; group I virus; ss
XX	
OS	Beet necrotic yellow vein mosaic virus.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..357
FT	/*tag= a
FT	/product= "P13 protein"
XX	
PN	WO200055301-A2.
XX	
PD	21-SEP-2000.
XX	
PF	07-MAR-2000; 2000WO-EP02176.
XX	
PR	12-MAR-1999; 99EP-0200773.
XX	
PA	(CNRS) CNRS CENT NAT RECH SCI.
XX	
PI	Jonard G, Lauber E, Guillely H, Richards K;
XX	
DR	WPI; 2000-602114/57.

DR P-PSDB; AAB18801.
 XX Inducing viral resistance into a plant or a plant cell, especially beet
 XX necrotic yellow vein virus-resistance into a sugar beet plant or cell
 XX by transforming the plant cell with triple gene block of the virus
 PS Disclosure: Fig 1; 27pp; English.
 XX
 CC The present sequence encodes a P13 protein of Beet necrotic yellow
 CC vein mosaic virus. The sequence is a triple gene block 2 (TGB2)
 CC sequence. It is used for inducing resistance to a group I virus. The
 CC method is useful for inducing resistance to a plant cell or plants
 CC such as sugar beet, potato, barley or peanut against group I virus
 CC such as hordeiviruses, benyviruses, pecluviruses and pomoviruses,
 CC preferably barley stripe mosaic virus, potato mop top virus, peanut
 CC clump virus and the beet soil-borne virus, more preferably beet
 CC necrotic yellow vein virus (BNYVV).
 XX
 SQ Sequence 357 BP; 89 A; 58 C; 93 G; 117 T; 0 other;
 Query Match 100.0%; Score 357; DB 21; Length 357;
 Best Local Similarity 100.0%; Pred. No. 6.1e-98;
 Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 1 ATGCTAGGGAATAACCGCTCGACCAATAGATGTCCTATTGTTGTTGTTGT 60
 Db 1 ATGCTAGGGAATAACCGCTCGACCAATAGATGTCCTATTGTTGTTGTTGT 60
 YY 61 GTTGCGCTTCTTTGATTTGCTGCTCATGACGACCAAAACATPAGACATCTGGG 120
 Db 61 GTTGCGCTTCTTTGATTTGCTGCTCATGACGACCAAAACATPAGACATCTGGG 120
 YY 121 GGTATTAACGAGTCCCAACATTTTCTAAGCGTGTATATATAGAGACGTCACAGATCA 180
 Db 121 GGTATTAACGAGTCCCAACATTTTCTAAGCGTGTATATATAGAGACGTCACAGATCA 180
 YY 181 GCTGATTTTATAGTAACATCATCGTGTACGGGTGCGGTCTGGGGTACCGTT 240
 Db 181 GCTGATTTTATAGTAACATCATCGTGTACGGGTGCGGTCTGGGGTACCGTT 240
 YY 241 AGTAGTCAGTGGGACCACTTATGTTAGTATGTTCTGTGTATATAGTGCA 300
 Db 241 AGTAGTCAGTGGGACCACTTATGTTAGTATGTTCTGTGTATATAGTGCA 300
 YY 301 CTATTACAAGCATTAAGGTCTCCACAGACACATTTGTAATGCTGTGGTTAA 357
 Db 301 CTATTACAAGCATTAAGGTCTCCACAGACACATTTGTAATGCTGTGGTTAA 357
 RESULT 2
 AAA75878
 ID AAA75878 standard; DNA: 357 BP.
 XX
 AC AAA75878;
 DT 22-JAN-2001 (first entry)
 XX
 DE DNA encoding a P13 variant of Beet necrotic yellow vein mosaic virus.
 KM P13 protein; triple gene block 2; TGB2; resistance; group I virus; ss.
 XX
 OS Beet necrotic yellow vein mosaic virus.
 XX
 FH Key Location/Qualifiers
 FT 1..357
 FT CDS /product="P13 protein"
 XX
 PN WO20005301-A2.
 XX 21-SEP-2000.
 XX
 PF 07-MAR-2000; 2000MO-EP02176.

XX
 FR 12-MAR-1999; 99EP-0200773.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Jonard G, Lauber E, Guilley H, Richards K;
 XX
 DR WPI: 2000-602114/57.
 DR P-PSDB; AAB18802.
 XX
 CC The present sequence encodes a P13 protein variant of Beet necrotic
 CC yellow vein mosaic virus. The P13 sequence is a triple gene block 2
 CC (TGB2) sequence. It is used for inducing resistance to a group I virus.
 CC The method is useful for inducing resistance to a plant cell or plants
 CC such as sugar beet, potato, barley or peanut against group I virus
 CC such as hordeiviruses, benyviruses, pecluviruses and pomoviruses,
 CC preferably barley stripe mosaic virus, potato mop top virus, peanut
 CC clump virus and the beet soil-borne virus, more preferably beet
 CC necrotic yellow vein virus (BNYVV).
 XX
 SQ Sequence 357 BP; 84 A; 60 C; 96 G; 117 T; 0 other;
 Query Match 97.3%; Score 347.4; DB 21; Length 357;
 Best Local Similarity 98.3%; Pred. No. 4.9e-95;
 Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 YY 1 ATGCTAGGGAATAACCGCTCGACCAATAGATGTCCTATTGTTGTTGTTGT 60
 Db 1 ATGCTAGGGAATAACCGCTCGACCAATAGATGTCCTATTGTTGTTGTTGT 60
 YY 61 GTTGCGCTTCTTTGATTTGCTGCTCATGACGACCAAAACATPAGACATCTGGG 120
 Db 61 GTTGCGCTTCTTTGATTTGCTGCTCATGACGACCAAAACATPAGACATCTGGG 120
 YY 121 GGTATTAACGAGTCCCAACATTTTCTAAGCGTGTATATATAGAGACGTCACAGATCA 180
 Db 121 GGTATTAACGAGTCCCAACATTTTCTAAGCGTGTATATATAGAGACGTCACAGATCA 180
 YY 181 GCTGATTTTATAGTAACATCATCGTGTACGGGTGCGGTCTGGGGTACCGTT 240
 Db 181 GCTGATTTTATAGTAACATCATCGTGTACGGGTGCGGTCTGGGGTACCGTT 240
 YY 241 AGTAGTCAGTGGGACCACTTATGTTAGTATGTTCTGTGTATATAGTGCA 300
 Db 241 AGTAGTCAGTGGGACCACTTATGTTAGTATGTTCTGTGTATATAGTGCA 300
 YY 301 CTATTACAAGCATTAAGGTCTCCACAGACACATTTGTAATGCTGTGGTTAA 357
 Db 301 CTATTACAAGCATTAAGGTCTCCACAGACACATTTGTAATGCTGTGGTTAA 357
 RESULT 3
 AAF26890
 ID AAF26890 standard; DNA: 739 BP.
 XX
 AC AAF26890;
 DT 09-APR-2001 (first entry)
 XX
 DE Beet necrotic yellow vein virus promoter sequence SEQ ID NO:2.
 XX
 KM Beet necrotic yellow vein virus; BNYVV; transformed plant;
 KW Rhizomania disease-resistant plant; promoter; ds.
 XX
 OS Beet necrotic yellow vein mosaic virus.
 XX
 PN JP2000312540-A.

PD 14-NOV-2000.
 XX 28-APR-1999; 99JP-0122628.
 XX 28-APR-1999; 99JP-0122628.
 XX (HOKK-) HOKKAIDO PREFECTURE.
 PA (HOKK-) HOKKAIDO TENSAN KYOKAI SH.
 XX WPI: 2001-054202/07.
 DR A Rhizomania disease-resistant plant -
 XX
 PS Claim 15; Page 9; 11pp; Japanese.
 XX
 CC The present invention describes a method for producing a transformed
 CC plant in which resistance against beet necrotic yellow vein virus
 CC (BNYVV) is given by transforming expressably a gene derived from BNYVV
 CC genome or a DNA corresponding to its part or a DNA substantially same
 CC as it in a plant genome. The vector structure can be used for
 CC transforming a plant or a plant cell having BNYVV resistance. The
 CC present sequence represents a mutant BNYVV promoter nucleotide
 CC sequence for use in the method of the invention.
 CC
 SQ Sequence 739 BP; 182 A; 117 C; 187 G; 253 T; 0 other;
 Query Match 91.0%; Score 325; DB 22; Length 739;
 Best Local Similarity 94.4%; Pred. No. 3.7e-88;
 Matches 337; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGCTTAGGAAATACCCCTGAGCCCAATAGATGTCCTATTGTTGTTGTTGT 60
 Db 1 ATGCTTAGGAAATACCCCTGAGCCCAATAGATGTCCTATTGTTGTTGTTGT 60
 QY 61 GTTGGCTTTCTTTGATTTGCTGGCTCATGAGCAAAACATAGACATTCCTGGG 120
 Db 61 GTTGGCTTTCTTTGATTTGCTGGCTCATGAGCAAAACATAGACATTCCTGGG 120
 QY 121 GGTGATTAACGAGTCCCAATTTCTAACGGTGTATATATAGAGACGCTACAGATCA 180
 Db 121 GGTGATTAACGAGTCCCAATTTCTAACGGTGTATATATAGAGACGCTACAGATCA 180
 QY 181 GCTGATTTTAATAGTACATATGCTTACGGGTGGGTGGTGGGTGAGCGTT 240
 Db 181 GCTGATTTTAATAGTACATATGCTTACGGGTGGGTGGTGGGTGAGCGTT 240
 QY 241 AGTAGTCAGTTGGGACGACACTATTGTTAGTATGTTCTGTTAAATAGTCTCA 300
 Db 241 AGTAGTCAGTTGGGACGACACTATTGTTAGTATGTTCTGTTAAATAGTCTCA 300
 QY 301 CTATTACAACGATTAAGTCTCCACAGAACACATTTGTATGCTGTTGTTAA 357
 Db 301 CTATTACAACGATTAAGTCTCCACAGAACACATTTGTATGCTGTTGTTAA 357
 RESULT 6
 ABR86954
 ID ABR86954 standard; cDNA; 507 BP.
 XX
 AC ABR86954;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Potato mop-top virus (PMTV) triple-gene-block (TGB-2 cDNA.
 XX
 KM Potato; antiviral; triple-gene-block 2; TGB-2; PMTV;
 KM Potato mop-top virus; Potomavirus; spiraling; dwarfing; mopping;
 KM chlorotic chevron; necrotic chevron; blotching; tuber cracking;
 KM necrotic conchoidal layer; viral movement; transgenic; molecular marker;
 KM resistance; agriculture; gene; ss.
 XX
 XX Potato mop-top virus.

FH Key Location/Qualifiers
 FT 37..396
 FT CDS /*tag= a
 FT /product= "TGB-2"
 XX
 XX WO200250281-A1.
 XX
 XX 27-JUN-2002.
 XX
 XX 18-DEC-2001; 2001WO-SE02805.
 XX
 XX 21-DEC-2000; 2000SE-0004755.
 XX
 XX (PLAN-) PLANT SCI SWEDEN AB.
 XX
 XX Melander M, Lee M;
 XX WPI: 2002-508804/54.
 XX P-PSDB; AAU79576.
 DR
 DR
 DR
 PT Nucleic acid molecule for producing plants with increased resistance
 PT against infection by potato mop-top virus comprises a structural gene
 PT encoding a triple-gene-block 2 polypeptide from the virus -
 PT
 XX
 XX Disclosure; Page 31; 36pp; English.
 CC
 CC The invention discloses a nucleic acid molecule comprising a promoter
 CC operably linked to a structural gene encoding a triple-gene-block 2
 CC (TGB-2) polypeptide from potato mop-top virus (PMTV) which differs from
 CC the wild-type polypeptide at a number of residues. The potato crop
 CC (Solanum tuberosum) is susceptible to PMTV which belongs to the genus
 CC Potomavirus. The main symptoms of the disease are spiraling, dwarfing
 CC (mopping), chlorotic and necrotic chevrons, blotching and tuber cracking
 CC and necrotic conchoidal layers. PMTV has a tripartite RNA genome, of
 CC which RNA 2 encodes for four proteins in a triple-gene-block and all
 CC three seem to be responsible for long-distance viral movement within the
 CC plant. The mutant TGB-2 is useful for producing transgenic plants, in
 CC particular, the potato plant, with an increased resistance against
 CC infection by PMTV. Portions of the mutant TGB-2 are useful as molecular
 CC markers for detecting a transgenic plant and for detecting a food product
 CC from the transgenic plant. The advantage the mutant TGB-2 brings is that
 CC it is able to render potato plants resistant by using solely a single
 CC gene which is easy to follow and maintain during a breeding program. The
 CC transgenic plants can be grown even in fields infected by PMTV, which
 CC increases the economic value of the yield obtained from such an infected
 CC field. The sequence presented is the wild-type TGB-2 cDNA from PMTV.
 CC
 XX
 SQ Sequence 507 BP; 143 A; 94 C; 106 G; 164 T; 0 other;
 Query Match 15.1%; Score 53.8; DB 24; Length 507;
 Best Local Similarity 57.5%; Pred. No. 2.6e-06;
 Matches 119; Conservative 0; Mismatches 82; Indels 6; Gaps 1;
 QY 6 TAGGAAATAACCGTCGACCCCAATAGATGTCCTATTGTTGTTGTTGTTGT 65
 Db 48 TAACGAAATTTGAGCGCGCAACCAATATATGTCGCGGAGTGTGCGAGTATGA 107
 QY 66 GGCCTTTCTTTGATTTGCTGGGCTTCATCAGCAAAACATAGACATTCCTGGGGTTA 125
 Db 108 TTGCTTTTGGTTTAAACAGTTACCAATCAAAACAGCTACTCATTCAGGTGATTA 167
 QY 126 TTACGAGTCCCAACATTTCTAACGCTGTATATATAGAGCGGTACAGATCA 185
 Db 168 TA-----TACATAATTTGCTAACGCTGGCTGTACAGGAGCGGTTCTAAGATATTAA 221
 QY 186 TTTTAATAGTAAACATCATGCTGCTTA 212
 Db 222 GTATTAATTTGATTAATTCACAGAGCTTA 248
 RESULT 7
 ABR86955
 ID ABR86955 standard; cDNA; 507 BP.

XX AC ABK86955;
 XX 24-SEP-2002 (first entry)
 XX DE Mutant potato mop-top virus (PMTV) triple-gene-block (TGB)-2 cDNA.
 XX KM Potato: antiviral; triple-gene-block 2; TGB-2; PMTV; 13kDmut;
 KM potato mop-top virus; Pomovirus; spraing; dwarfing; moping;
 KM chlorotic chevron; necrotic chevron; blotching; tuber cracking;
 KM necrotic conchoidal layer; viral movement; transgenic; molecular marker;
 KM resistance; agriculture; gene; ss; mutant.
 XX OS Potato mop-top virus.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FH CDS 37..396
 FT mutation /*tag= a
 FT mutation /product= "TGB-2 mutant (13kDmut)"
 FT mutation /tag= b
 FT mutation /tag= c
 FT mutation /tag= d
 FT mutation /tag= e
 FT mutation /tag= f
 FT mutation /tag= g
 FT mutation /tag= h
 FT mutation /tag= i
 FT mutation /tag= j
 XX MO200250281-A1.
 XX PD 27-JUN-2002.
 XX PF 18-DEC-2001; 2001WO-SE02805.
 XX PR 21-DEC-2000; 2000SE-0004755.
 XX PA (PLAN-) PLANT SCI SWEDEN AB.
 XX PI Melander M, Lee M;
 XX DR WPI: 2002-508804/54.
 XX DR P-PSDB: AAU79577.
 XX PT Nucleic acid molecule for producing plants with increased resistance
 PT against infection by potato mop-top virus comprises a structural gene
 XX encoding a triple-gene-block 2 polypeptide from the virus -
 XX Example 3; Page 32; 36pp; English.
 XX The invention discloses a nucleic acid molecule comprising a promoter
 CC operably linked to a structural gene encoding a triple-gene-block 2
 CC (TGB-2) polypeptide from potato mop-top virus (PMTV) which differs from
 CC the wild-type polypeptide at a number of residues. The potato crop
 CC (Solanum tuberosum) is susceptible to PMTV which belongs to the genus
 CC Pomovirus. The main symptoms of the disease are spraing, dwarfing
 CC and necrotic conchoidal layers. PMTV has a tripartite RNA genome, of
 CC which RNA 2 encodes for four proteins in a triple-gene-block and all
 CC three seem to be responsible for long-distance viral movement within the
 CC plant. The mutant TGB-2 is useful for producing transgenic plants, in
 CC particular, the potato plant, with an increased resistance against
 CC infection by PMTV. Portions of the mutant TGB-2 are useful as molecular

CC markers for detecting a transgenic plant and for detecting a food product
 CC from the transgenic plant. The advantage the mutant TGB-2 brings is that
 CC it is able to render potato plants resistant by using solely a single
 CC gene which is easy to follow and maintain during a breeding program. The
 CC transgenic plants can be grown even in fields infected by PMTV, which
 CC increases the economic value of the yield obtained from such an infected
 CC field. The sequence presented is a mutant TGB-2 (13kDmut) cDNA from PMTV.
 XX SQ Sequence 507 BP; 145 A; 95 C; 104 G; 163 T; 0 other;
 Query Match 12.8%; Score 45.8; DB 24; Length 507;
 Best Local Similarity 55.1%; Pred. No. 0.00067;
 Matches 114; Conservative 0; Mismatches 87; Indels 6; Gaps 1;
 QY 6 TAGGGAATTAACCGCTGACCCCAATTAAGATGTCCTATTGTTGCTGTTGTG 65
 DB 48 TAACGAATTTGGAGCGCGACCAATTAATATTTGGCGGTAGTTGTGCAAT 107
 QY 66 GGCCTTCTTTGATTTGCTGCGCTTCATGCAAGCAAAAACATTAAGACATTTGCGGCTGA 125
 DB 108 TTGCTTTTGGGTTTAAACAGTTTACCAATCAAAAACAGCTACATCAAGTGATTA 167
 QY 126 TTACGGAGTCCCAACATTTTCTAACGTTGTATATATTAAGAGAGGTACAGATCAGCTGA 185
 DB 168 TA-----TACATTAATTTGCTTAAGCTGCCGATTCAGGAAGCTGTAAGATTTAA 221
 QY 186 TTTTAATAGTAACAATCATGTCCTTA 212
 DB 222 GTATTAATGTATTAATTAATCCAGAGCTTA 248
 RESULT 8
 AAH34822
 ID AAH34822 standard; cDNA; 4039 BP.
 XX AAH34822;
 XX DT 03-SEP-2001 (first entry)
 XX DE Human colon cancer antigen encoding cDNA SEQ ID NO:1904.
 XX KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
 XX KM colorectal carcinoma; ss.
 XX OS Homo sapiens.
 XX PN WO200122920-A2.
 XX PD 05-APR-2001.
 XX PF 28-SEP-2000; 2000WO-US26524.
 XX PR 29-SEP-1999; 99US-0157137.
 XX PR 03-NOV-1999; 99US-0163280.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX DR WPI: 2001-235357/24.
 XX DR P-PSDB: AAG75417.
 XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 XX useful for preventing, diagnosing and/or treating colorectal cancers -
 XX Claim 1; Page 3415-3417; 9803pp; English.
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate p

expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 5544 BP; 1504 A; 1281 C; 1157 G; 1602 T; 0 other:

Query Match 10.3%; Score 36.6; DB 24; Length 5544;
Best Local Similarity 49.7%; Pred. No. 0.95;
Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

123 TGATTACGAGAGTCCCAACATTTCTTAACGGTGTATATATAGAGACGGTACACATCAGC 182
1106 TGACCCCTGGGACCAACACCCGCGAGTACTGTGACTTCCAAAGCCAGACACATGTGC 2165
183 TGATTATATAGTACATATCATGCTGCTTACGGGTGGGGTCTGGGGTACGCTTAG 242
2166 TCATCAAACTTGATTAAGCAGTTGGGAGATGCTGTGAGCTGGGGTTTAAGTGA 2225
243 TAGTCAGTTGGGACCAACTTATTTGTTAGCTATTTCTGTATATATAGTGTCACT 302
2226 TGGTCTCTTTTCTCCCTCTTTTGAAGGTAAAGCTACTGCTTCTTAAGAGTATTT 2285
303 ATTACAA 309
2286 ATGCCAA 2292

RESULT 12

AAS87055 standard; cDNA; 5549 BP.

AAS87055;
13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #22859.

Human: chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dymanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

P-PSDB; ABG22868.

New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
Claim 1; SEQ ID No 22859; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for treating
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 5549 BP; 1510 A; 1285 C; 1154 G; 1600 T; 0 other:

Query Match 10.3%; Score 36.6; DB 23; Length 5549;
Best Local Similarity 49.7%; Pred. No. 0.95;
Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

123 TGATTACGAGAGTCCCAACATTTCTTAACGGTGTATATATAGAGACGGTACACATCAGC 182
1106 TGACCCCTGGGACCAACACCCGCGAGTACTGTGACTTCCAAAGCCAGACACATGTGC 2165
183 TGATTATATAGTACATATCATGCTGCTTACGGGTGGGGTCTGGGGTACGCTTAG 242
2166 TCATCAAACTTGATTAAGCAGTTGGGAGATGCTGTGAGCTGGGGTTTAAGTGA 2225
243 TAGTCAGTTGGGACCAACTTATTTGTTAGCTATTTCTGTATATATAGTGTCACT 302
2226 TGGTCTCTTTTCTCCCTCTTTTGAAGGTAAAGCTACTGCTTCTTAAGAGTATTT 2285
303 ATTACAA 309
2286 ATGCCAA 2292

RESULT 13

ABK40083 standard; DNA; 1668 BP.

ABK40083;

21-MAY-2002 (first entry)

Human chemically pretreated gene sequence #83 strand 1.

Human: ds; disulphite treatment; CpG; DNA methylation; cancer; tumour;

KW cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; PTD; EPRX2; OCLN; TXNND1;

KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

Homo sapiens.

WO200202806-A2.

10-JAN-2002.

29-JUN-2001; 2001WO-EP07470.

30-JUN-2000; 2000DE-1032529.

01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

Human; immune system disease; cytosine methylation; antisthmatic;
arteriosclerosis; antineoplastic; cytoskeletal; neoplastic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
neurohumoral; anticholinergic; antidiabetic; antiparasitic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
gene; ds.

QY	3	GTGTAGGGAATAATACCGCGACGCCCAATTAAGAAATGTGCCCTAATGTGTTGGCGTTTGAGT	62
Db	3443	GTAATGGTGAATAATTTCCTTTTTCACGAAAAATACAAAAAATACGTTGGGCTGTGGTGGCGGTG	3507
QY	63	TGTGGCTTTCCTTTTGTAATTCCTGCTGCGCTTCATGCAAGCAAAAAACATAAGACACATTCCTGGGGG	122
Db	3503	TCTATATATTTTACTGTTATTTTGGGATGTTGAGGTAAAGGAAATCCTTTCAATCGACGAGCGGG	3562
QY	123	TGATTTACGAGATGCCAACATTTTCTAACGGTGTATATATAGACACGGTACACAGATCAGC	182
Db	3563	AGGTTGTACTGATGATCGAGATTCGTATATGTAATTTTACGTTGGGAAAGACAGATGAGATTT	3622
QY	183	TGATTTTAAATAGTACAAATCATCGGCTTA	212
Db	3623	TGTTTAAATTAATTAATTAATTAATTAATTA	3652

PD 18-OCT-2001

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XX 06-APR-2001; 2001WO-EP03970.
PF
XX
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-010922/01.
XX
XX New nucleic acid derived from chemically treated metastasis genes,
XX useful for diagnosis of cancers by analysis of cytosine methylation,
XX also for treatment
XX
PS Claim 1; SEQ ID NO 108; 23pp + Sequence Listing; English.
XX
CC The present invention provides a number of human metastasis associated
CC genes which are modified by cytosine methylation. The sequences can be
CC used in the diagnosis and treatment of cancer. The present sequence is
CC one of the genes of the invention.
XX
SQ Sequence 6725 BP; 2074 A; 53 C; 1429 G; 3169 T; 0 other;
Query Match 10.0%; Score 35.6; DB 24; Length 6725;
Best Local Similarity 48.1%; Pred. No. 2;
Matches 101; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
OY * 3 GTCAGGGAATATACCCCTGCACCAATAGAGATGTCCTATTGTTGTTGTTGT 62
DB 3443 GTATGGTGAATTCGTTTTCGAAAAATAGAAAAATTAGTTGGGTGTTGGTG 3502
OY 63 TGTGGCTTCTTTTGTATGCTGCGGTCATGCAGCAAAACATAAGACACATTCTGGGG 122
DB 3503 TTTATATTTTATGTTATTTGGAGTGTGAGTAGAGAAATCGTTGAATCGAGAGGCGG 3562
OY 123 TGATTACGAGAGTCCCAACATTTTCTAACGCTGTATATATAGACAGCGTACAAGATCAGC 182
DB 3563 AGGTTGTAGTGCAGTGCAGATGTGTATTTGTTAGTTTGGAAAGAGAGTGAATTT 3622
OY 183 TGATTTAATAGTAACATCATCGTCTTA 212
DB 3623 TGTTTAATATATATATATATATATA 3652

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Search completed: March 12, 2003, 08:17:17
 Job time : 189 secs

GenCore version 5.1.4_P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: March 11, 2003, 10:26:12 ; Search time 53.5 Seconds
(without alignments)
2046.423 Million cell updates/sec

Title: US-09-936-011-1

Perfect score: 357
Sequence: 1 atgctctagggaataaccgc.....gtcaatgctgtgtgttaa 357

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	30.8	8.6	2848	3	US-08-539-205A-3
2	30.4	8.5	799	4	US-09-149-476-288
3	30.4	8.5	1847	4	US-09-149-476-149
4	30.4	8.5	1847	4	US-09-149-476-287
5	30.4	8.5	9595	3	US-09-014-416-4
6	29.6	8.3	4285	4	US-09-410-464-1
7	29.2	8.2	11309	4	US-08-961-527-108
8	29	8.1	1370	4	US-09-026-408-12
9	29	8.1	1371	4	US-09-026-408-1
10	29	8.1	1857	4	US-09-138-001C-332
11	28.8	8.1	2362	1	US-08-920-812-5
12	28.8	8.1	2362	1	US-08-920-812-5
13	28.8	8.1	2362	1	US-08-921-177-5
14	28.8	8.1	2362	1	US-08-362-577C-5
15	28.8	8.1	2362	2	US-08-920-828-5
16	28.8	8.1	5883	1	US-08-404-445-1
17	28.8	8.1	6060	5	PCT-US96-09430-7
18	28.8	8.1	8442	4	US-09-272-032-6
19	28.6	8.0	875	4	US-08-936-165A-125
20	28.6	8.0	1506	2	US-08-663-566A-8
21	28.6	8.0	1506	2	US-08-023-610-8
22	28.6	8.0	1506	2	US-08-288-065A-8
23	28.6	8.0	1506	2	US-08-362-240A-8
24	28.6	8.0	1506	4	US-08-804-372A-6
25	28.6	8.0	1506	5	PCT-US95-10245-8
26	28.6	8.0	1825	5	US-09-071-035-463
27	28.6	8.0	2601	3	US-09-039-773A-2

28	28.6	8.0	6168	4	US-09-071-035-457	Sequence 457, App
29	28.6	8.0	6168	4	US-09-071-035-461	Sequence 461, App
30	28.6	8.0	6168	4	US-09-071-035-465	Sequence 465, App
31	28.4	8.0	660	4	US-09-549-804C-1	Sequence 1, Appl1
32	28.4	8.0	2910	4	US-09-206-942-31	Sequence 31, Appl1
33	28.4	8.0	2928	4	US-09-206-942-29	Sequence 29, Appl1
34	28.4	8.0	3454	4	US-08-961-527-207	Sequence 207, App
35	28.4	8.0	16569	4	US-09-097-889-2	Sequence 2, Appl1
36	28.4	8.0	16569	4	US-09-377-856-1	Sequence 1, Appl1
37	28.4	8.0	16569	4	US-09-302-681-2	Sequence 2, Appl1
38	28.4	8.0	18596	4	US-09-318-448-11	Sequence 11, Appl1
39	28.2	7.9	1170	5	PCT-US96-05320A-900	Sequence 900, App
40	28.2	7.9	5511	3	US-08-928-361B-2	Sequence 2, Appl1
41	28.2	7.9	7334	1	US-08-928-361B-1	Sequence 1, Appl1
42	28	7.8	549	1	US-08-196-945-1	Sequence 1, Appl1
43	28	7.8	846	2	US-08-743-637B-189	Sequence 189, App
44	28	7.8	7766	4	US-09-125-619-3	Sequence 3, Appl1
45	27.8	7.8	2087	4	US-09-097-199-83	Sequence 83, Appl1

ALIGNMENTS

RESULT 1
US-08-539-205A-3
Sequence 3, Application US/08539205A
Patent No. 6001619
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Uridylytin ligases, and uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2848 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 238..2535
US-08-539-205A-3
Query Match 8.6%; Score 30.8; DB 3; Length 2848;
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 77; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
5 CTAGGGAATTAACCGCTGACCCCAATAGATGTGCTTGTGTGTGTGTGTGTG 64

Db 377 CTATCAAAAAGACGTTAAACCCATTATGGATGAGACTTTGAAGTAAATGTTACAGATA 436
Qy 65 TGGCTTCTTTGATTGCTGGCGTTTCATGCAGCAAAAACATAGACACATTCGGGGTG 124
Db 437 ATAGACACCATGCGATTCAGGTGTTTCATGCAGCAAAAATTTAAGAAAAAGGCCAAGGCT 496
Qy 125 ATTACGAGTCCCAACATTTTCTAACGGTGGTAT 158
Db 497 TTCTAGGAGTGATTAATCTTCTGTTGGAGATGT 530

RESULT 2
US-09-149-476-288
Sequence 288, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
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EARLIER APPLICATION NUMBER: 60/040,336
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
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EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864

34 AATGCGCCTATTGTTGTTGGCTTTCTTGTATTCCTGGCGTTCATG 93

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612

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US-09-149-476-287			
Sequence 287, Application US/09149476			
Patent No. 6420536			
GENERAL INFORMATION:			
APPLICANT:	Kosen et al.		
TITLE OF INVENTION:	166 Human Secreted proteins		
FILE REFERENCE:	P200291		
CURRENT APPLICATION NUMBER:	US/09/149,476		
CURRENT FILING DATE:	1998-09-08		
EARLIER APPLICATION NUMBER:	PCT/US98/04493		
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36	EARLIER FILING DATE: 1997-08-22
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49	EARLIER APPLICATION NUMBER: 60/056, 903
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53	EARLIER APPLICATION NUMBER: 60/056, 879
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056, 880
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056, 894
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056, 911
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056, 636
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056, 874
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056, 910
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/056, 864
68	EARLIER FILING DATE: 1997-08-22
69	EARLIER APPLICATION NUMBER: 60/056, 631
70	EARLIER FILING DATE: 1997-08-22
71	EARLIER APPLICATION NUMBER: 60/056, 845
72	EARLIER FILING DATE: 1997-08-22
73	EARLIER APPLICATION NUMBER: 60/056, 892

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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Query Match 8.5%; Score 30.4; DB 4; Length 1847;
Best Local Similarity 61.2%; Pred. No. 3.4; Mismatches 31; Indels 0; Gaps 0;
Matches 49; Conservative 0;

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QY 34 AATGTCCTATTGTTGGTGTGTTGCTTCTTGTGTAATGCTGCGCTCANG 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1734 AACATACCTTAGTCTTTGTTGTTTGTGTTTGTGTTTGTCTTATG 1793
QY 94 CAGCAAAACATAGACACA 113
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Db 1794 AAGAAATAAATAAGTCA 1813
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RESULT 5
US-09-014-416-4
; Sequence 4, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Buhk, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; EARLIER FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 9595
; ORGANISM: Hepatitis C virus
US-09-014-416-4
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Query Match 8.5%; Score 30.4; DB 3; Length 9595;
Best Local Similarity 61.2%; Pred. No. 7.2; Mismatches 31; Indels 0; Gaps 0;
Matches 49; Conservative 0;

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QY 1 ATGCTAGGGAATACCGCTCGACCAATAGATGCTTATGTTGGTGTGTTGT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9371 ATGACGGGAGGCTAACACACGCGCTTACGCAATTCCTGTTTCTTTT 9430
QY 61 GTTGTGCTTCTTCTTATG 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9431 TTTTCTTTCTTTCTTTT 9450
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RESULT 6
US-09-410-464-1
; Sequence 1, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-1
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Query Match 8.3%; Score 29.6; DB 4; Length 4285;
Best Local Similarity 54.6%; Pred. No. 9; Mismatches 49; Indels 0; Gaps 0;
Matches 59; Conservative 0;

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QY 175 AGATCAGCTGATTTAATAGTAACATCATGCTTACGGGTGGGCTGCGGCT 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2340 AATCAGGTAATCTCAAGAAATACCTTCATATATGCAATGCTATGTTTAT 2599
QY 235 AGCGTAGTAGTCGAGTGGCGACCACTAATGTTAGCTATTGTT 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2600 GGGAATATCTGTAATTTGTGGAGCTACTAATTAAGTATTGTTT 2647
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ZIF: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..1242
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 109..1242
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 67..108
US-09-026-408-1
Query Match 8.1%; Score 29; DB 4; Length 1371;
Best Local Similarity 54.1%; Pred. No. 8.4;
Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
OY 241 AGTAGTCAGTTGGCAGCAGCACTTATGCTGTAAGTATGTTCTGTAATAGTCA 300
DB 57 AGAAGTCAAAAGGACACATCTTCTTGAGCTCTTCTATGCTGTTTGGAGTCA 116
OY 301 CTATTACAAGCATTAAGTCTCCACGACACATTTGTAATGTCCTT 349
DB 117 AGCTCAAGATGCTCAGCTCAAAAAAATACGGAATTTGGAGTGCCTT 165
RESULT 10
US-09-134-001C-332/C
Sequence 332, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 332
LENGTH: 1857
TYPE: DNA
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-332
Query Match 8.1%; Score 29; DB 4; Length 1857;
Best Local Similarity 51.1%; Pred. No. 9.6;
Matches 68; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
OY 71 TCTTTGATGTCGGCGCTGACGCAAAACATAGACATTCGGGGTGATTAAG 130
DB 260 TGTCCTATTGAGAAATATATGATTAAGCGCATTAACGTTAATGTCTATCTCC 201
OY 131 GAGTCCCAACATTTTCTAAGCGTGCTATATAGACGGTACAAAGATCAGCTATTTTA 190
DB 200 GCTTGGAACACCCCATGATGAGTTGACCTTGATATGAGCTTCACTGTTTAA 141
OY 191 ATAGTACATCA 203
DB 140 ATGTACTGAACA 128
RESULT 11
US-08-920-812-5
Sequence 5, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-3
US-08-920-812-5
Query Match 8.1%; Score 28.8; DB 1; Length 2362;
Best Local Similarity 51.1%; Pred. No. 12;
Matches 93; Conservative 0; Mismatches 87; Indels 2; Gaps 1;

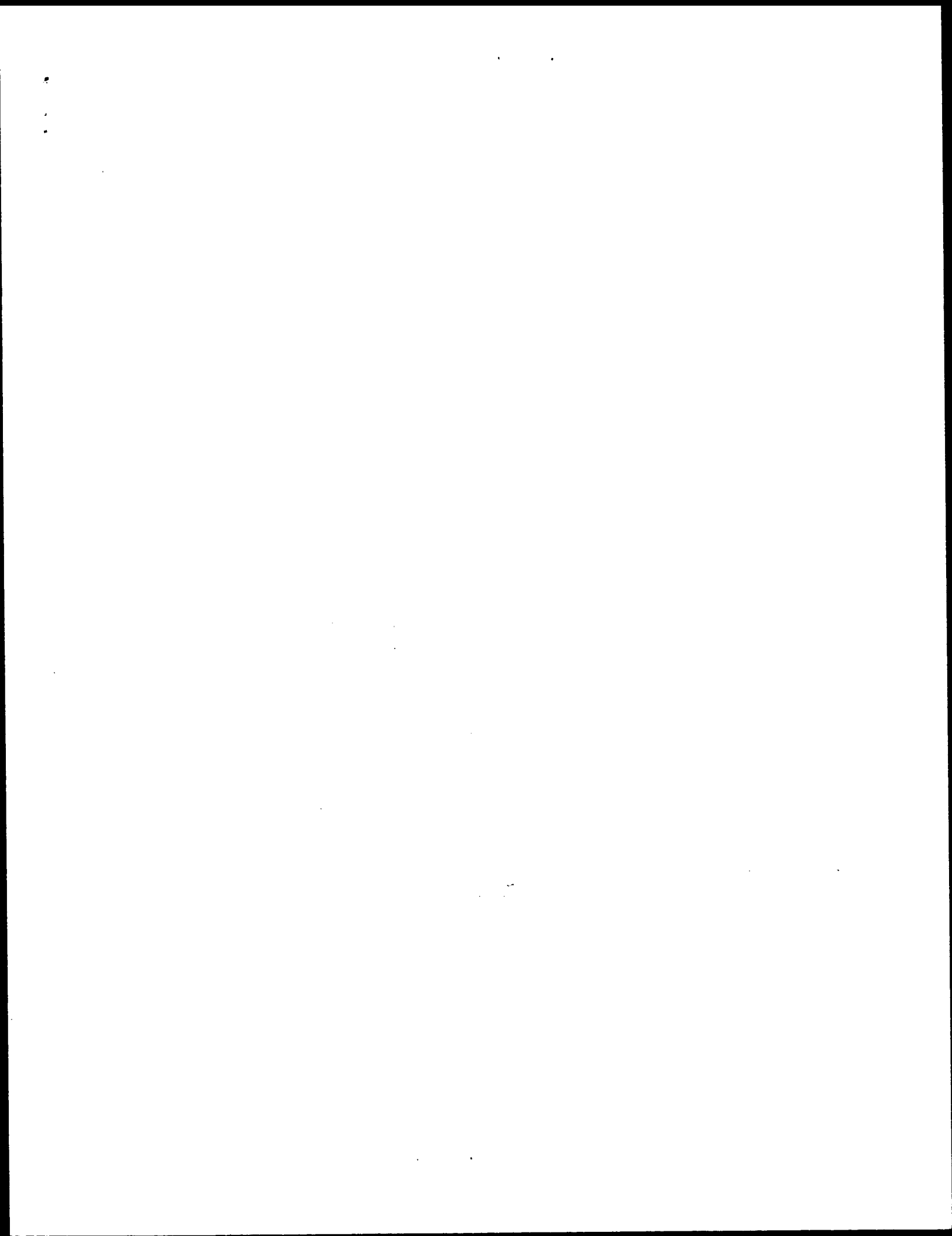
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Page 11

Oy 199 AA 200
11
Db 1254 AA 1255

Search completed: March 11, 2003, 15:25:54
Job time : 72.5 secs




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Query Match          9.0%: Score 32.2; DB 10; Length 234;
Best Local Similarity 46.9%: Pred. No.2.3;
Matches 100; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 27 CAATAAGAAATGCGCTAATGCTTGTGTGATGTTTGTGCTTGCCCTTCTTGTATGCTGAC 86
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 CACTTACTTGTACTTATTTATGAAACAGTCTGTCGTACATGACCAACTTTGGCTATGATGA 162

QY 87 GTTATGACGACAAAACATAAGACACATTTGGGGGGTATTACGGAGTCCCAACATTTTC 146
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 TGACTAGAGAAAGATGATGATGCTGATGATAGTAGTAGTGAACATATGATAGTGTGG 102

QY 147 TTAACGTGCTTATTTATATGAGACGCTACAAAGATCAAGCTATTTTATATGTAACATATCG 206
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 TGAATGATAGTATGTTATGATGACGATGGTGGTATGATGATATTTGATGGTGACAGTAA 42

QY 207 TGCCTTACGGGTGCGGTGGGCTCTGGGGGTACGCGT 239
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 TGGTGTGTGTAGTGTGATGATGATGATGATGATGCTGT 9

RESULT 5
US-09-938-842A-892/c
/ Sequence 892, Application US/09938842A
/ Patent No. US20020160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kreps, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ TITLE OF INVENTION: SAME, AND METHODS OF USE
/ FILE REFERENCE: SCRIPI300-3
/ CURRENT APPLICATION NUMBER: US/09/938, 842A

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	Query Match	8.9%;	Score 31.8;	D8 9;	Length 1126;	
	Best Local Similarity	53.7%;	Pred. No. 5.9;			
Matches	66;	Conservative	0;	Mismatches	57;	Indels
					0;	Gaps
OY	12 AATAACGCGCTGCACCCAATAGCATGTGCTATTGTGGTGTGGTGTTGGTCCTTT	71				
Db	841 AAGAAGCTCCGCATGTAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	782				
OY	72 CTTGTATTGCTGGCGGTCATCGACAAAACATTAAGCACATTTCGGGGGTATTACGG	131				
Db	781 CATGTGCTTGATGTGGATTTCAGCAGAAAGAGAGAGACACTTTGAAGGCCAATTCCT	722				
OY	132 AGT 134					
Db	721 TGT 719					

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RESULT 6
US-09-887-576--68/c
; Sequence 68, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,652
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-887-576-68

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Query Match	8.9%	Score 31.8	DB 10	Length 2000
Best Local Similarity	53.7%	Pred. No. 7.5		
Matches	66	Conservative	0	Mismatches 57
				Indels 0
				Gaps 0
QY	12	AATAACCGCTCGACCCACATAGAATATGCCCATATGTTGTCGTGTGTCGGCGTT	71	
Db	522	AAGAAGCTGCCATGATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	463	
QY	72	CTTTGTAATTCCTGGCGTTTCATGCAGCAGCAAAACATAMAGACATCTGGGCGATTACGG	131	
Db	462	CATGTGGTTATATGTGATTTTGACACAGAAGAGAGACAGCATTTTGACTCGCCAATTTCCCT	403	


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Query Match      8.7% ; Score 31; DB 10; Length 753;
Best Local Similarity 62.0% ; Pred. No. 8.7;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0.

QY      36  TGTGCGTATTGTGTGTGTGCTGTGTTGCTGCTTCCTTTGATATGCTGCGCTTCATGCA 95
          |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      593  TGTCATCAATAGTGTGTGGTCTTGTGTTTGTGTTTGTTCCTTTGGATCTTGTTCAT 652

QY      96  GCATCAATCATACACACAT 114
          |||  ||| ||| ||| ||| |||
Db      653  GCACCTTAGATATGGAAAT 671

RESULT 12
US-09-764-864-676
; Sequence 676, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864

```


Thu Mar 13 12:38:20 2003

us-09-936-011-1.rnpb

Page 7

D**b** 1089 AACATACCCTTAAGTGTGTTTGTTGGTTTTGTTTCCTTAGC 1148
Oy 94 CAGCAAAAAACATAAGCACACA 113
 ||||| | | |
D**b** 1149 AAGAATAAATAAAATTAGTCA 1168

Search completed: March 12, 2003, 08:11:06
Job time : 749 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2003, 06:32:01 ; Search time 1191.5 Seconds
(without alignments)
4852.529 Million cell updates/sec

Title: US-09-936-011-1

Perfect score: 357
Sequence: 1 atgtctagggaataaccgc.....gtaatgctgtctgtgtaaa 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_estbta:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42.4	11.9	1080	17	CNS00EPP
2	42.2	11.8	1101	17	CNS00L72
3	38.6	10.8	1101	17	CNS0178M
4	38	10.6	375	9	AJ388997
5	38	10.6	1101	17	CNS0100X
6	37.2	10.4	367	17	AQ090830

7	36.6	10.3	873	14	BO215809
8	36.6	10.3	1007	17	CNS0079A
9	36.4	10.2	486	9	AA134045
10	36	10.1	328	10	BB224881
11	36	10.1	1101	17	CNS00FOO
12	35.8	10.0	902	17	CNS0060P
13	35.6	10.0	1207	17	CNS0152N
14	35.2	9.9	501	17	AQ447722
15	35.2	9.9	529	13	BT743894
16	35.2	9.9	554	17	AO523013
17	35	9.8	884	17	CNS0060U
18	35	9.8	922	17	CNS0073W
19	35	9.8	994	17	CNS00F9Q
20	34.8	9.7	1101	17	CNS00100
21	34.6	9.7	477	14	BO353390
22	34.6	9.7	894	12	BB76437
23	34.6	9.7	939	17	CNS00CNG
24	34.4	9.6	504	17	AO529268
25	34.4	9.6	552	17	AZ400908
26	34.4	9.6	587	12	BE921791
27	34.4	9.6	598	13	BJ033222
28	34.4	9.6	612	17	AG159078
29	34.4	9.6	645	17	AG000861
30	34.4	9.6	660	14	BO112425
31	34.4	9.6	691	14	BO112425
32	34.4	9.6	720	12	BF863620
33	34.4	9.6	721	13	BJ137716
34	34.4	9.6	781	9	AA849835
35	34.4	9.6	1017	13	BT161612
36	34.2	9.6	401	10	BB671302
37	34.2	9.6	605	17	DR20K6S
38	34.2	9.6	665	17	AZ863079
39	34.2	9.6	910	17	CNS06JMH
40	34	9.5	228	9	AU073823
41	34	9.5	254	9	AV240878
42	34	9.5	325	9	AU271393
43	34	9.5	673	17	AG066509
44	34	9.5	1101	17	CNS006DU
45	33.8	9.5	418	17	B43757

ALIGNMENTS

RESULT 1
LOCUS CNS00EPP
DEFINITION Drosophila melanogaster genome survey sequence TE73 end of BAC: BACR29N07 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL069494.1 GI:4949637
VERSION
KEYWORDS
SOURCE
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1080)

REFERENCE
AUTHORS
TITLE
JOURNAL
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammaster in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

OY	222	TGGGCTGTGGGGGATAGCGTGTAGTCAGTGTTGGCAGACACTATTGTGTACTACTATGT	281
Dd	686	KKKGCTGGDGSKKAKGBRAMAMRAKATRTAAADATATAATTAKAATMTKTTKTTT	745
OY	282	TTCGTGTATATAGTGCATCATATTACAAGATTAAAGTCCACCAGAACACATTTGTAA	341
Dd	746	KTTTTTTTTTTTCKTTTARAKNRDRDDDKAKRKDGDKDGDMDADKMKAKAGRDRDDPFKMG	805
OY	342	TGGTCTTGTGTGTTA	357
Dd	806	WKDRAGKKKKKKKH	821
RESULT 6			
LOCUS	AO909830	367 bp	DNA linear GSS 09-JAN-2001
DEFINITION	GSSFC08309 Trypanosoma cruzi random genomic library Trypanosoma		
ACCESSION	AO909830		
VERSION	AO909830.3	GI:10135556	
KEYWORDS	GSS.		
SOURCE	Trypanosoma cruzi.		
ORGANISM	Trypanosoma cruzi Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;		
REFERENCE	Trypanosoma; Schizotrypanum. 1 (bases 1 to 367)		
AUTHORS	Aguero,F., Verdin,R., Frasch,A.C.C. and Sanchez,D.O.		
TITLE	A random sequencing approach for the analysts of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery		
JOURNAL MEDLINE	Genome Res. 10 (12), 1996-2005 (2000) 20368489		
COMMENT	On Sep 14, 2000 this sequence version replaced gi:9374600. Contact: Sanchez D.O. Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)		
FEATURES	Source location/Qualifiers		
	1..367		
	/organism="Trypanosoma cruzi"		
	/strain="Cl-Bremer"		
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	/clone="g37j17"		
	/clone_1lb="Trypanosoma cruzi random genomic library"		
	/cell_type="epimastigote"		
	/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 kb range was gel purified and cloned into the dephosphorylated HindIII site of the vector"		
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ORIGIN			
Query Match	10.4%; Score 37.2; DB 17; Length 367;		
Best Local Similarity	54.3%; Pred. No. 25;		
Matches	75; Conservative 0; Mismatches 63; Indels 0; Gaps 0;		
OY	33	GAAATGCCATTATGTTGGTGGTGTGTGTGTTGTCCTTCTTGATTCGTGCGCTTCAT	92
Dd	114	GAAGTACTTTTTTTTGGTGCGCGTGTGTGTGTTGTTGTTGTTGTTGTTGTTGA	173
OY	93	GCAGCAAAAACATTAAGCACATTTCTGGGGGCGATTAAGGAGTCCCACAATTTCTAACG	152
Dd	174	TACTCAAAACAAACAAAAAAGAGAGGAAAAACAATTCCTTTTTTTTTTTTCGG	233

	QY	153	TGCTATATATAGACGGG	170	
	Db	234	GTCGACGAGGAGAGGG	251	
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RESULT 7					
LOCUS	BQ215809		873 bp	mRNA	linear EST 02-MAY-2002
DEFINITION	AGENCOURT_7574890 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059837				
ACCESSION	BQ215809				
VERSION	BQ215809.1		GI:20397219		
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	1 (bases 1 to 873)				
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs@email.nih.gov				
	Tissue Procurement: DCTD/DTP/Gazdar				
	cDNA library Preparation: Life Technologies, Inc.				
	DNA Sequencing by: Agencourt Bioscience Corporation (LNL)				
	Clone distribution: MGC Clone Distribution Information can be				
	found through the I.M.A.G.E. Consortium/LNL at:				
	http://image.lnl.gov				
	Plate: ILAM1327 row: c column: 06				
FEATURES	High quality sequence stop: 645.				
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	/db_xref="taxon:9606"				
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	/note="Organ: Lung; Vector: pCMV-Sport6; Site_1: NotI;				
	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.				
	Average insert size 1.8 kb. Library constructed by Life				
	Technologies."				
BASE COUNT	203 a 224 c 162 g 284 t				
ORIGIN					
	Query Match 10.3%; Score 36.6; DB 14; Length 873;				
	Best Local Similarity 49.7%; Pred. No. 36;				
	Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;				
QY	123 TGAATTAGGAGTGCCCACATTTTCTAAGCGGTATATATAGAGAGGATACAAGTCAGC	182			
Db	33 TGACCCCCCTGGCACCAACACC GCCAGACTGTGACTTCCAAGA GCAGACCAATGTGC	92			
QY	183 TGAATTTAATAGTAACATCATCGTGTCTTAGCGGTGCGGTGGGTGACCTTAG	242			
Db	93 TCATCAAACTTGCACTTAAGCAGTGGCGGAGATGGCTGTGAGCTGGGGGTTAATGA	152			
QY	243 TAGTCGAGTTGGCGAGCAACTAATGTGTAGACTAATGTTCTGTCTTAATAGTCACT	302			
Db	153 TGGTCTCTTGTGCTCCCTCTTTGAGGGATAAGCTACTGCTCTCTTAAGAGTGAATT	212			
QY	303 ATTACAA 309				
Db	213 ATGCCAA 219				
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RESULT 8					
LOCUS	CNS0079A/c		1007 bp	DNA	linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC #				

SOURCE	Magnaporthe grisea.
ORGANISM	Magnaporthe grisea Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE	1 (bases 1 to 501)
AUTHORS	Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
JOURNAL	Unpublished (1998)
COMMENT	Contact: Dean RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Email: rdean@clemson.edu Seq primer: TAATACGACTCAGCTATGCGG Class: BAC ends High quality sequence stop: 357.
FEATURES	location/Qualifiers 1..501 /organism="Magnaporthe grisea" /strain="70-15" /db_xref="taxon:148305" /clone="mgxb0010K03f" /clone_1id="CUGI Rice Blast BAC library" /tissue_type="Protoplasts" /lab_host="E. coli DH10B" /note="vector: pBACWICH; Site.1: HindIII; Site.2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
BASE COUNT	173 a 107 c 103 g 118 t
ORIGIN	
Query Match	9.9%; Score 35.2; DB 17; Length 501;
Best Local Similarity	52.0%; Pred. No. 82;
Matches	79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY	25 CCCAATTAAGAATGGCCATTGTGTTGGTGTGTTGGCTTCTTGTATTGCTG 84
DB	185 CCGAACAAATGGGTTTTTTATTGTTTGTGTTGGATCGGCCATTATCGTTGGTT 126
QY	85 GCGTTCATGCAGCAAAAACATAAGACACATTCCTGGGGGTGATTACGGAGTCCACATTT 144
DB	125 TCTGTAACTATTCGGCAAAACCCATTAACAAAGAAAGTAAAAATAGACCCCAACGGTC 66
QY	145 TCTAACGGTGTATATATAGACGGTACAAG 176
DB	65 TCTGGCGTTGCTCTCAATAATAGACGTGTCAG 34
RESULT 15	
LOCUS	B1743894 529 bp mRNA linear EST 25-SEP-2001
DEFINITION	Kx42c08.y1 Parastromyloides trichosuri FL PAMP1 v1 Chlaell11
ACCESSION	MCcarter Parastromyloides trichosuri cDNA 5' similar to TR:09VND9
VERSION	09VND9 CG1753 PROTEIN.;, mRNA sequence.
KEYWORDS	B1743894.1 GI:15765696
SOURCE	EST.
ORGANISM	Parastromyloides trichosuri. Parastromyloides trichosuri Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panafroloimoidae; Strongyloidiidae; Parastromyloides.

```

REFERENCE
AUTHORS
1 (bases 1 to 529)
McCarteer,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisshvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harrey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,K., Waterston,R. and
Wilson,R.
TITLE
The Washington Univ. Nematode EST Project, 1999
JOURNAL
Unpublished (1999)
COMMENT
Contact: McCarteer JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wuston.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarteer (bchiapel@wuston.wustl.edu & jmccarte@wuston.wustl.edu) at
Washington University, St. Louis. DNA sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 395.
FEATURES
Source
1..529
Location/Qualifiers
/organism="Parastromyloides trichosuri"
/db_xref="taxon:131310"
/clone_lib="Parastromyloides trichosuri FL PAMP1 v1
Chiapelli McCarteer"
/dev_stage="Free Living"
/lab_host="DH10B"
/note="vector: PAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
The library was constructed by Brandi Chiapelli and Dr.
James McCarteer at Washington University, St. Louis. The
cDNA was made by using Dynabead oligo-dT priming (Dynaf)
PCR based library using a modified protocol from the
SMART PCR cDNA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of PAMP1. Nematodes were
provided by Dr. Warwick Grant of AgResearch, New Zealand
(warwick.grant@agresearch.co.nz)."
BASE COUNT
201 a 67 c 107 g 134 t
ORIGIN
Query Match 9.9%; Score 35.2; DB 13; Length 529;
Best Local Similarity 48.5%; Pred. No. 82;
Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0.
70 TTCTTTGATTTGCTGCGCTTCATGCACAAAACATTAAGACACATTCCTGGGGTGATTAC 129
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 115 TTGTTATTGGTGCAGAACTGAGGAACAGTAAACAGAAATTGGAAAAAAATTTAAAGAA 174
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Qy 130 GGAGTCCCAACATTTTCTAACGGGTGATATATAGAGACGCTCAAGATCAGCTGATTTT 189
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Db 175 AGAGTTCCAACATGTCAAATTTGTTGGTCAGATTCAGAAAGTTCATATTATAGTAACCC 244
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Qy 190 AATAGTAAACATATGCTGCTTACGGGGTGGGTGGCTGGGGGTACGCTTACTAGTCGA 249
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 235 GATATTAAACAATTCCTCATACGAAGTTGAAGGTACAGAGATATGATTTTGTCCAGCA 294
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Qy 250 GTTGGGCAGCACTTATGT 269
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db 295 GTTCTTGACAGAAAGTATGT 314
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 15:26:24 ; Search time 1159 Seconds

(without alignments)
8964.367 Million cell updates/sec

Title: US-09-936-011-3

Perfect score: 357
Sequence: 1 atgcttaggaataaccgc.....gtaatgctgcttggttaa 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	357	100.0	357	6	AX039060
2	347.4	97.3	357	6	AX039058
3	347.4	97.3	4612	14	TOBNVYV2
4	345.8	96.9	1922	14	BNVWTP1
5	328.2	91.9	739	6	ES9890
6	328.2	91.9	4544	14	AF197556
7	328.2	91.9	4609	6	ES9889
8	328.2	91.9	4609	14	BNVWTP2
9	323.4	90.6	4544	14	AF197547
10	321.8	90.1	1922	14	BNVWTP2
11	315.4	88.3	739	6	ES9891
12	208.2	58.3	4616	14	AF061869
13	65.4	18.3	3065	14	LVBABCD
14	59.6	16.7	3005	14	BSBV3GNS
15	53	14.8	3591	14	PSZBETACD
16	50.4	14.1	2529	14	BVQ223598
17	48.6	13.6	2417	14	D86638
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19	47.4	13.3	2962	14	PMO277556
20	46.2	12.9	3215	14	BSU35769
21	46.2	12.9	3237	14	BSU35772
22	46.2	12.9	3289	14	HOBSVVR
23	46	12.9	4290	14	AF239729
24	45.8	12.8	4504	14	PNMRNAT
25	45.6	12.8	204615	2	AC112254
26	44.6	12.5	3239	14	BSU35770
27	44.6	12.5	3249	14	BSU35771
28	43.2	12.1	32070	2	AC116983
29	42.4	11.9	2325	14	NVMV2
30	42	11.8	164140	2	AC106093
31	41	11.5	171438	2	AC099231
32	41	11.5	179846	2	AC119387
33	39.6	11.1	136587	9	AL445309
34	39.6	11.1	178870	2	AC023938
35	39.6	11.1	178870	2	AC021555
36	39.6	11.1	215738	2	AC113274
37	39.6	11.1	258120	2	AC114408
38	38.8	10.9	128433	2	AC124151
39	38.4	10.8	171031	2	AC104020
40	38.4	10.8	202504	2	AC127585
41	38	10.6	162312	2	AC114455
42	38	10.6	164422	2	AC095588
43	37.8	10.6	172076	2	AC121895
44	37.8	10.6	194158	2	AC107761
45	37.8	10.6	210824	2	AC126661

ALIGNMENTS

RESULT 1
LOCUS AX039060
DEFINITION Sequence 3 from Patent EP1038961.
ACCESSION AX039060
VERSION AX039060.1 GI:11228356
KEYWORDS
SOURCE
ORGANISM
Beet necrotic yellow vein virus.
Beet necrotic yellow vein virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
1 (bases 1 to 357)
REFERENCE
Lauber E., Jonard G., Guillely H. and Richards K.
METHOD for inducing viral resistance into a plant
Patent: EP 1038961-A 3 27-SEP-2000;
DE CENTRE NAT (FR)

FEATURES

Source

Location/Qualifiers

1..357

/organism="Beet necrotic yellow vein virus"

/db_xref="taxon:31721"

1..357

/note="unnamed protein product"

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BASE COUNT

84 a 60 c 96 g 117 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 357; DB 6; Length 357;

Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCTAGGGAATAACCGCTGACCCCAATAGATGCGCTATTGTTGTTGTTGT 60

QY 61 GTTGCGCTTTCTTTGATATGCTGCGCTTCAATGACGACGCTGACACATTCGGG 120

DB 61 GTTGCGCTTTCTTTGATATGCTGCGCTTCAATGACGACGCTGACACATTCGGG 120

QY 121 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 180

DB 121 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 180

QY 181 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 240

DB 181 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 240

QY 241 AGTAGTCGAGTGGGACGACACTTATGTTAGCATATGTTCTGTAAATAGTGTCA 300

DB 241 AGTAGTCGAGTGGGACGACACTTATGTTAGCATATGTTCTGTAAATAGTGTCA 300

QY 301 CTATTACAACGATTAGGCTCCACCAACATTTGTAATGCTGCTGTGTTAA 357

DB 301 CTATTACAACGATTAGGCTCCACCAACATTTGTAATGCTGCTGTGTTAA 357

RESULT 2

LOCUS AX039058 357 bp DNA linear PAT 16-NOV-2000

DEFINITION Sequence 1 from Patent EP1038961.

ACCESSION AX039058

VERSION AX039058.1 GI:11228354

KEYWORDS

SOURCE

ORGANISM

Beet necrotic yellow vein virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.

REFERENCE

1 (bases 1 to 357)

Lauber, E., Jonard, G., Guille, H. and Richards, K.

TITLE

Method for inducing viral resistance into a plant

JOURNAL

Patent: EP 1038961-A 1 27-SEP-2000;

DE CENTRE NAT (FR)

FEATURES

Source

Location/Qualifiers

1..357

/organism="Beet necrotic yellow vein virus"

/db_xref="taxon:31721"

1..357

/note="unnamed protein product"

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ORLRSPPHICNACG"

BASE COUNT

89 a 58 c 93 g 117 t

ORIGIN

Query Match

Best Local Similarity 97.3%; Score 347.4; DB 6; Length 357;

Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGCTAGGGAATAACCGCTGACCCCAATAGATGCGCTATTGTTGTTGTTGT 60

DB 1 ATGCTAGGGAATAACCGCTGACCCCAATAGATGCGCTATTGTTGTTGTTGT 60

QY 61 GTTGCGCTTTCTTTGATATGCTGCGCTTCAATGACGACGCTGACACATTCGGG 120

DB 61 GTTGCGCTTTCTTTGATATGCTGCGCTTCAATGACGACGCTGACACATTCGGG 120

QY 121 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 180

DB 121 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 180

QY 181 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 240

DB 181 GGTGATTACGAGTCCCAACATTTTCTAAGCTGTATATAGACGCTACAGATCA 240

QY 241 AGTAGTCGAGTGGGACGACACTTATGTTAGCATATGTTCTGTAAATAGTGTCA 300

DB 241 AGTAGTCGAGTGGGACGACACTTATGTTAGCATATGTTCTGTAAATAGTGTCA 300

QY 301 CTATTACAACGATTAGGCTCCACCAACATTTGTAATGCTGCTGTGTTAA 357

DB 301 CTATTACAACGATTAGGCTCCACCAACATTTGTAATGCTGCTGTGTTAA 357

RESULT 3

LOCUS TOBNYVV2 4612 bp RNA linear VRL 25-MAY-1999

DEFINITION Beet necrotic yellow vein virus RNA-2.

ACCESSION X04197

VERSION X04197.1 GI:62050

KEYWORDS

coat protein; subgenome; unidentified reading frame.

SOURCE

Beet necrotic yellow vein virus.

ORGANISM

Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.

REFERENCE

1 (bases 1 to 4612)

Bouzoubaa, S., Ziegler, V., Beck, D., Guille, H., Richards, K. and

AUTHORS

Jonard, G.

TITLE

Nucleotide sequence of Beet Necrotic Yellow Vein Virus RNA-2

JOURNAL

J. Gen. Virol. 67, 1689-1700 (1986)

COMMENT

Partial readthrough of the termination codon at position 709-711

gives rise to 75k protein

Data kindly reviewed (02-SEP-1987) by Bouzoubaa S.

FEATURES

Source

Location/Qualifiers

1..4612

/organism="Beet necrotic yellow vein virus"

/strain="isolate F13"

/db_xref="taxon:31721"

/clone="pBF14, pBC2"

1..8

/note="inverted repeat A"

27..34

/note="inverted repeat A"

145..2220

/note="75k protein (aa 1-691); read-through stop-codon"

/codon_start=1

/transl_except="(pos:709..711,aa:OTHER)

/protein_id="CAB43511.1"

/db_xref="GI:4894189"

/translation="MSSEGRYMTWKDMSHNKFMTRMARVSDVSVTKQSHAMLSKA
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NLTDGSLADNASAN/RDVSNGKNKASSTAGTNSAVTLVSLAGLAOLLEE
LMTDRKFEDEKRLPMTPVGGRSPQXOLAAARVTAHTAAKRALILYPCDSDPVG
WKHFYPPPYDVVDVPLDITINKLADDDIGGLVTP1PASSHGCLPEVSEVEEONRN
SLMTLVGLLALALAIIGVAYVHRKLIQSRLRELKLMGSTGGGGGGGFGTEHTRA
PTDVSIGTLSEHVAPASGLRHRPATDSGPHRELVPEVWVFNLAAYVDSIGMSDL
FYTAREVGVNDFEGGLIELLSPDDDDGYTAPDPTAIDAYSCENYRIDETV
LIERINLKKLLEAEALEREEREDMTMIADDEQRTLLHRLSESVAEAVHYTKARADA

RAAVALAALASKANDYDMSKAFDRSCKEQELRLLELVNSMPKTERVHTGOGGA
 QLAGAMAVGAMLRRASSSSQNVSGGANGSOLTRGRSASOPLSSVGGSTRGVNN
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CDS
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 /db_xref="GI:62051"
 /db_xref="SPTREMBL:088620"
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 LMTYRDKFEDERFKLPMTPVCGRTSPGQ"
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 /protein_id="CAA27792.1"
 /db_xref="GI:1334951"
 /db_xref="SPTREMBL:088621"
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 PLDIINAKLAADIGGLVPTPASSHGLPEVSEFEVQANRNSLMTGLLALAI
 GIGTAYHRRKIOSRLREIKLMGSTGSGGGGCTELHTRATDTVSLCTLSHVA
 PARGGLHRRPAATDSPEHVLPEVWVFDNLAVYDSIGMSDLEFTYVREPEVGESEF
 EGLEELSPDDDGVTYNAEDTAIDAYESQENYDRIDVETVLERRINILKLEEL
 AELEERRRDMTMIADDEORTLHRLLESRYEATVYVTKAEADARAVALMAALSKLEA
 DYSKMAFDRSCKEQELRLLELVNSMPKTERVHTGOGGAQLAGAMAVGAMLRG
 ASSSSQNVSGGANGSOLTRGRSASOPLSSVGGSTRGVNNINNTNLVFRAGNSA
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 213..3287
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 /protein_id="CAA27793.1"
 /db_xref="GI:62053"
 /db_xref="SPTREMBL:088659"
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 VIKTLVEDGYKMGVKGPHCHDMGKLESGAIDNFRGTLBELGKNCDLTGNAAVKL
 DTLOKVTSSDMTARVIGILGAPGVGKSTIKNLDFGAKHMYCLPFSOLLEGVF
 AGRLDFVLVDLFCRSYVEGKNTMLVDEYTRVHKCEILVLAGHLGVKNVTCFDPVQ
 GLNYKAGSAVNANPEPIIAECYASRRFGKATADLINSNGGKRPVGNNEVDSWTFEE
 LCGKILDSMTVLVAATRETOKFLEEDNISLSDAGQYDVVTLILEDEDDAALICD
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 3287..3643
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 /db_xref="GI:62054"
 /db_xref="SPTREMBL:088622"
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 VPFNSGCIYRDGTRSDPFSNNHRAVCGCGSGSVSSRVGOQLIVLAIYVLLVSL
 ORLRSPENICNACG"
 3627..4025
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 AGRLDFVLVDLFCRSYVEGKNTMLVDEYTRVHKCEILVLAGHLGVKNVTCFDPVQ
 GLNYKAGSAVNANPEPIIAECYASRRFGKATADLINSNGGKRPVGNNEVDSWTFEE
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 4025..4426
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 /codon_start=1
 /protein_id="CAA27796.1"
 /db_xref="GI:62056"
 /db_xref="SPTREMBL:088623"
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 GVCGCCSEFTLADEKPHVIVDEPV"
 4612

polYA_site
 BASE COUNT 1200 a 760 c 1209 g 1443 t
 ORIGIN

Query Match 97.3% Score 347.4: DB 14: Length 4612;
 Best Local Similarity 98.3%: Pred. No. 2.8e-92;
 Matches 351: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	ATGTCTAGGGAATTAACCGCTGACCAATAAGATGCTATTGTTGGTGTCT	60
DB	3287	ATGTCTAGGGAATTAACCGCTGACCAATAAGATGCTATTGTTGGTGTCT	3346
QY	61	GTGTGGCTTCTTGTATGCTGCTGCTCATGACGACGACGACGACATCTCTGG	120
DB	3347	GTGTGGCTTCTTGTATGCTGCTGCTCATGACGACGACGACGACATCTCTGG	3406
QY	121	GGTATTACGAGAGCCCAACATTTCTTACAGGTGTATATAGACGCTCAAGATCA	180
DB	3407	GGTATTACGAGAGCCCAACATTTCTTACAGGTGTATATAGACGCTCAAGATCA	3466
QY	181	GGTATTATTATAGTAAACATCATCTGCTTACGGGTCGGTGGGTAGCGTT	240
DB	3467	GGTATTATTATAGTAAACATCATCTGCTTACGGGTCGGTGGGTAGCGTT	3526
QY	241	AGTAGTCAGATGGGACGACAACTATTGTGTAGCTATTGTTCTGTATTAAGTCA	300
DB	3527	AGTAGTCAGATGGGACGACAACTATTGTGTAGCTATTGTTCTGTATTAAGTCA	3586
QY	301	CTATTACAGATTAAGGTCTCCACGACGACAACTTTGTAATGGTGTGCTTAA	357
DB	3587	CTATTACAGATTAAGGTCTCCACGACGACAACTTTGTAATGGTGTGCTTAA	3643

RESULT 4
 BNYMTP1
 LOCUS
 DEFINITION
 Beet necrotic yellow vein mosaic virus (RG1) genomic RNA for
 transport proteins.
 x75575
 x75575.1 GI:496548
 VERSION
 13k transport protein; 15k transport protein; 42k transport
 protein; transport protein.
 SOURCE
 Beet necrotic yellow vein virus.
 Beet necrotic yellow vein virus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Bunyavirus.
 1 (bases 1 to 1922)
 REFERENCE
 Koenig, R.
 Unpublished
 REMARK
 2 (bases 1 to 1922)
 AUTHORS
 Solov'yev, A.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (02-NOV-1993) Solov'yev A., Institute for Biochemistry and
 Plant Virology, Messweg 11/12, Braunschweig, Germany
 FEATURES
 source
 1..1922
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 /db_xref="taxon:31721"
 1..1155
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 LCGKILDSMTVLVAATRETOKFLEEDNISLSDAGQYDVVTLILEDEDDAALICD
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 /db_xref="GI:496550"
 /db_xref="SPTREMBL:088622"

CDS

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translation="MSRETTAPDNKKVPIVAGCVAAFPALLAFMOOKHHTSHSGDGV
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1495..1893
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/db_xref="GI:496551"
/db_xref="SPTREMBL:O08950"
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FTILISLRGLAVLEPMICLMSLYVMWYIHR"

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BASE COUNT	505 a	309 c	506 g	602 t
ORIGIN				

Query Match	96.9%	Score 345.8	DB 14	Length 1922
Best Local Similarity	98.0%	Pred. No. 8e-92		
Matches 350	Conservative 0	Mismatches 7	Indels 0	Gaps 0

QY	1	ATGCTAGGAAATATACCGTCGACCCATAGAGTATGCCATATGTTTGATGGTTTGT	60
Db	1155	ATGCTTAGGGAAATATACCGTCGACCCATAGAGTATGCCATATGTTTGATGGTTTGT	1214
QY	61	GTTGTGCTTCTTGTATATGCTGGCGTTATGACAGACAGCTGCACACATTTGTGGG	120
Db	1215	GTTGTGCTTCTTGTATATGCTGGCGTTATGACAGACACACATTTGTGGG	1274
QY	121	GGTGATTCAGCAGTCCCAACATTTCTTAAAGGTGTATATATAGAGACGTCACAAATCA	180
Db	1275	GGTGATTCAGCAGTCCCAACATTTCTTAAAGGTGTATATAGAGACGTCACAAATCA	1334
QY	181	GCTGATTTTAAATAGTAACATATGCTGCTTACGGGTGGCGGTGCTGGGGTACGGTT	240
Db	1335	GCTGATTTTAAATAGTAACATATGCTGCTTACGGGTGGCGGTGCTGGGGTACGGTT	1394
QY	241	AGTATCGAGTTGGGCAGCAACTTATTTGTTAGCTATTTGTTCTGTATATAGTGTCA	300
Db	1395	AGTATCGAGTTGGGCAGCAACTTATTTGTTAGCTATTTGTTCTGTATATAGTGTCA	1454
QY	301	CTATTACAAACGATTAAAGCTCTCACACAGAAACATTTGAATGCTCTGTGGTTTAA	357
Db	1455	CTATTACAAACGATTAAAGCTCTCACACAGAAACATTTGAATGCTCTGTGGTTTAA	1511

RESULT 5

LOCUS	E59890	739 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	Rhizomania-resisting plant.				

DEFINITION	Rhizomania-resisting plant.
ACCESSION	E59890
VERSION	E59890.1 GI:18622726
KEYWORDS	JP 2000312540-A/2.
SOURCE	Beet necrotic yellow vein virus.
ORGANISM	Beet necrotic yellow vein virus
REFERENCE	Viruses: ssRNA positive-strand viruses, no DNA stage; Benyvirus. 1 (bases 1 to 739)
AUTHORS	Nomura,S., Kamitani,G., Saito,M., Kiguchi,T., Kusu,S. and Soma,C.
TITLE	Rhizomania-resisting plant
JOURNAL	Patent: JP 2000312540-A 2 14-NOV-2000;
COMMENT	GENCHI KAMITANI,SHADANHOJIN HOKKAI TENSAN KYOKAI OS Beet necrotic yellow vein virus

PD	14-NOV-2000	
PF	28-APR-1999	JP 1999122628
PR		
PI	SHINJI NOMURA, GENICHI KAMITANI, MINAKO SAITO, TADAHIKO KIGUCHI,	
PI	SHUNZO KUSUME,	
PI	CHIHIRO SOMA	
PC	A01H5/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00	CC
FM	Key	
FT	Location/Qualifiers	
FT	source	
	1. .739	
	/organism=Beet Necrotic Yellow Vein Virus',	
	Location/Qualifiers	
	1. .739	
FEATURES		
source		

BASE COUNT	184	a	114	c	189	g	252	t
ORIGIN	/organism="Beet necrotic yellow vein virus" /db_xref="taxon:31721"							

Query Match	91.9%;	Score 328.2;	DB 6;	Length 739;
Best Local Similarity	95.0%;	Pred. No. 1.3e-86;		
Matches 339;	Conservative 0;	Mismatches 18;	Indels 0;	Gaps 0.

QY	1	ATGTCGTAGGGAATAATACCGCTGCAGCCCAATATAGAAATGAGCCATATATGTTGTTGGATGTTT	160
Db	1	ATGTCGTAGGGAATAATACCGCTGCAGCCCAATATAGAAATGAGCCATATATGTTGTTGGATGTTT	60
QY	61	GTTGTGGCTTCTTGTATATGTCGTGGCGTATATGAGCAACAGCTGGCGACACATTTCTGGG	120
Db	61	GTTGTGGCTTCTTGTATATGTCGTGGCGTATATGAGCAACACATATAGACACATTTCTGGG	120
QY	121	GGTGATTACGAGAGTCCCAACATTTTCTAACGGTGTATATATAGACAGGTACACATCA	180
Db	121	GGCGATTACGAGAGTCCCAACATTTTCTAACGGTGTATATATAGAGAGCGGTACAAAGTCA	180
QY	181	GCTGATTTTATATATACAAATCATCGTGCCTACGAGGGTGGCGGTGTGGGGGTAGCGTT	240
Db	181	GCTGATTTTATATATATATATCATATCATCGTGTCTTACGGGTGGCGGTGTGGGGGTAGCGTT	240
QY	241	AGTAGTCAGTTGGGCGACCACTATTGTGTAGCTATGTTTCTGTGTTAATATAGTCTCA	300
Db	241	AGTAGTCAGTGGGCGACCACTGTTGTGTATACCTATGTGTGTGTTAATATAGTATCA	300
QY	301	CTATTACACGATTAAGGTCTCCACCGAAGAACATTTGATATGGCTGTGGTTAA	357
Db	301	CTGTTACACGATTTAAGATCTCCACCGAAGAACATTTTGTATATGGTGTGGTTAA	357

RESULT 6
AE107556

Accession	LOCUS	DEFINITION
AF197556	4544 bp	RNA linear
	Beet necrotic yellow vein virus isolate Kas3	VRL 04-DEC-2000
		RNA 2 segment, partial

ACCESSION	sequence.
VERSION	AF197556
KEYWORDS	AF197556.1 GI:11528045
SOURCE	.
ORGANISM	Beet necrotic yellow vein virus.
REFERENCE	Beet necrotic yellow vein virus.
AUTHORS	Viruses: ssRNA positive-strand viruses, no DNA stage; Benyvirus.
TITLE	1 (bases 1 to 4544)
	Koenig, R. and Lemmings, B. L.
	Molecular analyses of European A, B and P type sources of Beet
	yellow vein virus and detection of the rare P type in

REFERENCE 2 (bases 1 to 4544)

DIRECT SUBMISSION
 TITLE
 Submitted (21-OCT-1999) Institut fuer Pflanzenvirologie,
 JOURNAL Mikrobiologie und Biologische Sicherheit, Biologische Bundesanstalt
 fuer Land und Forstwirtschaft, Messeweg 11, D 38104 Braunschweig D
 38104, Germany
 Location/Qualifiers

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FEATURES
    source
        location/Qualifiers
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                /isolate="Kas3"
                /db_xref="taxon:31721"
                /country="Kazakhstan"
                /note="closely related to P type
                    almost complete sequence of RNA 2: lacks only a few
                    nucleotides at the 5' and 3' ends
                    type: P; segment: RNA 2"
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                /codon_start=1

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LMWRPFKEDRLKWPVQGRTPSPGQDLAARVYAHAAKRALLYGDSPEWGM
KHPPPPDYDVPLDIINAKLAADDIGLVTPTPASSHGLPEFEVSEBOANRS
LMLTGLLLAALAVIGVAAVYHKKLOSRLRELKLMGSGSGGGGPDTELMBAT
DVSGLTLEHAASAPSGLRHAPATDSGPHEALPEFVAMPDNLISVVDSTGMSDL
VTVREVFVNGEPEGLIELLESPDDOSVYNNAPDRTAIDAESEQENDRIDITFL
LERRNLKLLLEAELEERERDRTMADEORTLHRLSESVETATHAVAKADAR
AAVATLALASKEANDYDSKMAFDRSCQEGELRLRELEVMSPEKTERVYHTGOGAO
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671..673
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movement"
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movement"
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/translation="MSREITARPKNRPPIVGVYAEFVLLAFMOOKKHTSGGDY
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3586..3984
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movement"
/codon_start=1
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/db_xref="GI:11528049"
/translation="MVLVVKVYDLNIVLYIAGCVVSMKLYSPFSSNDVKASVAGV
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4002..4385
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/protein_id="AAG37096.1"
/db_xref="GI:11528050"
/translation="MGWVDSLCEVFRVYITEGSESVESVERSIKFESEKMLLTAVY
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GYGDCSESTLADKXHNHIVDPVY"
BASE COUNT 1174 a 756 c 1207 g 1407 t
ORIGIN
Query Match 91.9% Score 328.2; DB 14; Length 4544;
Best Local Similarity 95.0% Pred. No. 1.4e-86;
Matches 339; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATAACCGCTGACCAATAAGATGTCCTATTGTTGGTGTGTT 60
|||||
DB 3246 ATGCTAGGGAATAACCGCTGACCAATAAGATGTCCTATTGTTGGTGTGTT 3305
|||||
QY 61 GTTGTGCTTCTTGTATGCTGCGTTCAAGCAAGCGCTGCGACATCTGCG 120
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Db 3306 GTTGTGCTTCTTGTATGCTGCGTTCAAGCAAGCAAGCAATACATCTGCG 3365
QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGGTATATATAGACGGTACAGATCA 180
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Db 3366 GCGGATTACGAGTCCCAACATTTCTTAACGGTGGTATATAGACGGTACAGATCA 3425
QY 181 GCTGATTTAATAGTACATATCATGCTTACGGGTGGGCGGTCTGGGGGTACGCTT 240
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Db 3426 GCTGATTTAATAGTACATATCATGCTTACGGGTGGGCGGTCTGGGGGTACGCTT 3485
QY 241 AGTAGTCAGTTGGGCGACCAACTATTGTAGTATTGTTCTGTGTAATAGTGTCA 300
|||||
Db 3486 AGTAGTCAGTTGGGCGACCAACTATTGTAGTATTGTTCTGTGTAATAGTGTCA 3545
QY 301 CTATTACACAGTTAAGTCTCCACCAACATTTGTAATGCTGCTGTGTTAA 357
|||||
Db 3546 CTGTTACACAGTTAAGTCTCCACCAACATTTGTAATGCTGCTGTGTTAA 3602

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RESULT 7

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LOCUS E59889 4609 bp DNA linear PAT 31-JAN-2002
DEFINITION Rhizomania-resisting plant.
ACCESSION E59889
VERSION E59889.1 GI:18622725
KEYWORDS JP 2000312540-A/1.
SOURCE Beet necrotic yellow vein virus.
ORGANISM Beet necrotic yellow vein virus.
REFERENCE 1 (bases 1 to 4609)
AUTHORS Nomura,S., Kamitani,G., Saito,M., Kiguchi,T., Kusu,S. and Some,C.
TITLE Rhizomania-resisting plant
JOURNAL Patent: JP 2000312540-A 14-NOV-2000;
GENICHI KAMITANI, SHADANHOJIN HOKKAIDO TENSUAI KYOKAI
OS Beet necrotic yellow vein virus
PN JP 2000312540-A/1
PD 14-NOV-2000
PE 28-APR-1999 JP 1999122628
PR
PI SHINJI NOMURA, GENICHI KAMITANI, MINAKO SAITO, TADAHIKO KIGUCHI,
PI SHUZO KUSOME,
PI CHIHIRO SOMA
PC A01H5/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
FH key Location/Qualifiers
FT source 1..4609
FT location/Qualifiers
FT "organism"=Beet necrotic yellow vein virus"

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Location/Qualifiers
"organism"=Beet necrotic yellow vein virus"
/db_xref="taxon:31721"

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BASE COUNT 1187 a 765 c 1221 g 1436 t
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Best Local Similarity 95.0% Pred. No. 1.4e-86;
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Db 3284 ATGCTAGGGAATAACCGCTGACCAATAAGATGTCCTATTGTTGGTGTGTT 3343
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QY 61 GTTGTGCTTCTTGTATGCTGCGTTCAAGCAAGCGCTGCGACATCTGCG 120
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QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGGTATATAGACGGTACAGATCA 180
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Db 3404 GGTGATTACGAGTCCCAACATTTCTTAACGGTGGTATATAGACGGTACAGATCA 3463
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QY 181 GCTGATTTAATAGTACATATCATGCTTACGGGTGGGCGGTCTGGGGGTACGCTT 240
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Db 3464 GCTGATTTAATAGTACATATCATGCTTACGGGTGGGCGGTCTGGGGGTACGCTT 3523
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QY 241 AGTAGCGAGTGGGCGACACTATGTTAGCTATGTTCTGTATAGTACGCA 300
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 RESULT 8
 LOCUS BNYKPRO2
 DEFINITION BNYKPRO2 4609 bp RNA linear VRL 06-FEB-1999
 protein, 15k protein, 14k protein, 75k protein.
 ACCESSION
 VERSION D84411.1 GI:1304018
 KEYWORDS coat protein; pot. 54k protein; 75k protein; 14k protein; 15k protein; 13k protein; 42k protein.
 SOURCE Beet necrotic yellow vein virus (isolate: S, lab_host: Tetragonia expansa) cDNA to genomic RNA, clone: 145-1, H20, S4, S7, PMPCRD5, PMPCRSX19, PMRP70, PMSD25.
 ORGANISM Beet necrotic yellow vein virus
 VIRUSES; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 REFERENCE
 AUTHORS Saito M., Kiguchi T., Kusume T. and Tamada T.
 TITLE Complete nucleotide sequence of the Japanese isolate S of beet necrotic yellow vein virus RNA and comparison with European isolates
 JOURNAL Arch. Virol. 141 (11), 2163-2175 (1996)
 MEDLINE 9712891
 REFERENCE
 AUTHORS Saito M., Kiguchi T., Kusume T. and Tamada T.
 TITLE Complete nucleotide sequence of a Japanese isolate S of beet necrotic yellow vein virus and comparison with European isolates
 JOURNAL unpublished
 REFERENCE
 AUTHORS Kiguchi T.
 TITLE 3 (bases 1 to 4609)
 JOURNAL Direct Submission
 REFERENCE
 AUTHORS Submitted (12-APR-1996) Tadahiko Kiguchi, Hokkaido Central Agricultural Experiment Station, Plant Biotechnology, Higashi 6 Kita 15, Naganuma, Hokkaido 069-13, Japan (tel: 01238-9-2001, Fax: 01238-9-2060)
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 /isolate="S"
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 BASE COUNT 1187 a 765 c 1221 g 1436 t
 ORIGIN
 Query Match 91.9%; Score 328.2; DB 14; Length 4609;
 Best Local Similarity 95.0%; Pred. No. 1,4e-86;
 Matches 339; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 1 ATGCTAGGAAATATACCGCTGACCAATTAAGATGCTATGTTGTTGTTGT 60
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 DB 3404 GCGGATTACGAGATCCCAATTTTCTAAGCGGTGTATATAGACGATACAGATCA 3463
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 DB 3464 GGTGATTAAATAGTAATATATATCATCGTCTTACGGGTGCGGTGGGTCTGGGGTAGCGTT 3523
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 QY 241 AGTAGCGAGTGGGCGACACTATGTTAGCTATGTTCTGTCTGTATAGTACGCA 300
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 DB 3524 AGTAGCGAGTGGGCGACACTATGTTAGCTATGTTCTGTCTGTATAGTACGCA 3583
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 QY 301 CTATTCAACGATTAAGTCTCCACGACACATTTGTAATGCTGTGTTAA 357
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 DB 3584 CTGTTCACGATTAAGTCTCCACGACACATATTGTAATGCTGTGTTAA 3640
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 RESULT 9
 LOCUS AF197547
 DEFINITION Beet necrotic yellow vein virus isolate F75 RNA 2 segment, partial
 4544 bp RNA linear VRL 04-DEC-2000

Accession	Sequence
AF197547	AF197547.1 GI:11528023
Source	Beet necrotic yellow vein virus.
Organism	Beet necrotic yellow vein virus
Reference Authors	Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus. 1 (bases 1 to 4544)
Title	Koenig, R. and Lennette, B. L. Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan
Journal	Arch. Virol. 145 (8), 1561-1570 (2000)
Medline	20456802
PubMed	11003469
Reference Authors	2 (bases 1 to 4544)
Journal Title	Koenig, R. Direct Submission
Features	Submitted (21-OCT-1999) Institut fuer Pflanzenvirologie, Mikrobiologie und Biologische Sicherung, Biologische Bundesanstalt fuer Land und Forstwirtschaft, Messeweg 11, D 38104 Braunschweig D 38104, Germany
Source	Location/Qualifiers
	1. 4544
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	/isolate="F75"
	/db_xref="taxon:31721"
	/country="France"
	/note="almost complete sequence of RNA 2; lacks only a few nucleotides at the 5'- and 3'-ends
	type: P; segment: RNA 2"
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	/note="first triple gene block; necessary for virus movement"
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QY 1	ATGCTAGGGAATPACCGCTGCAGCCCAATAGAAATGCTATTTGTTGGTGTGTTGT 60	
Db 3246	ATGCTTAGGGAAATPACCGCTGCAGCCCAATAGAAATGCTATTTGTTGGTGTGTTGT 3305	
QY 61	GTTGTGCTTCTTCTGTATGCTGGCGTTATGACGAAGAAGCTGGACACATTCGCG 120	
Db 3306	GTTGTGCTTCTTCTGTATGCTGGCGTTATGACGAAGAAGCTGGACACATTCGCG 3365	
QY 121	GCTGATTTAATAGTAACAATATCATGCTGCTTACAGCGTGTATATAGACAGCTACAAGATCA 180	
Db 3366	GCGCGATTCAGGAGTCCCAACATTTTCTAACGCTGGTAATATAGAGACGCCACAAGCTCA 3425	
QY 181	GCTGATTTAATAGTAACAATATCATGCTGCTTACAGCGTGTATATAGACAGCTACAAGATCA 240	
Db 3426	GCTGATTTAATAGTAACAATATCATGCTGCTTACAGCGTGTATATAGAGACGCCACAAGCTCA 3485	
QY 241	AGTACTCGAGTTGGGACCAACTATTGTGTAGCTATTCTTCTGTGTAAATAGTGCAC 300	
Db 3486	AGTACTCGAGTGGGACCAACTATTGTGTAGCTATTCTTCTGTGTAAATAGTGCAC 3545	
QY 301	CTATTACACAGATTATAGTCTCCACACAGACACATTTGTAATGTCGTCGTTGTTAA 357	
Db 3546	CTGTTACACAGATTATAGTCTCCACACACATTTGTAATGTCGTCGTTGTTAA 3602	
RESULT 10		
LOCUS	BNYVMP2	1922 bp RNA linear VRL 01-AUG-1994
DEFINITION	Beet necrotic yellow vein mosaic virus (Yu2) genomic RNA for transport proteins.	
ACCESSION	BNYVMP2	
VERSION	X75574.1	GI:496552
KEYWORDS	13k transport protein; 15k transport protein; 42k transport protein; transport protein.	
SOURCE	Beet necrotic yellow vein virus.	
ORGANISM	Beet necrotic yellow vein virus.	
REFERENCE	1 (bases 1 to 1922)	
AUTHORS	Kruse, M., Koenig, R., Hoffmann, A., Kaufmann, A., Commandeur, U., Solovjev, A.G., Savchenko, I. and Burgermeister, W.	
TITLE	Restriction fragment length polymorphism analysis of reverse transcription-PCR products reveals the existence of two major strain groups of beet necrotic yellow vein virus	
JOURNAL	J. Gen. Virol. 75 (Pt 8), 1835-1842 (1994)	
MEDLINE	94321971	

PUBMED REFERENCE AUTHORS TITLE JOURNAL	
7913953 2 (bases 1 to 1922) Solooyev, A. Direct Substitution Submitted (02-NOV-1993) Solooyev A., Institute for Biochemistry and Plant Virology, Messweg 11/12, Braunschweig, Germany Location/Qualifiers 1. .1922	

BASE COUNT	505 a	309 c	509 g	599 t	ORIGIN
Query Match	90.1%;	Score 321.8;	DB 14;	Length 1922;	
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Db	1155	ATGCTTAGGGAATAAACCCGCTCGACCCATAAGAAAGTGCTATTGTTGGTGTTGTT	1214		
QY	61	GTGTGGCTTCTTGTATTGTGCGCGTTCATGCACACAACAGACAGGTGGACATCTGGG	120		
Db	1215	GTGTGGCTTCTTGTATTGTGCGCGTTCATGCACACAAAACATAAGACACATGCTGGG	1274		
QY	121	GCTGATTACGGAGATCCCAACATTTTCTAAAGGTGTATATATAGAGACGGTAAAGATCA	180		
Db	1275	GCGGATTACGGAGATCCCAACATTTTCTAAAGGTGTATATATAGAGACGGTAAAGATCA	1334		
QY	181	GCTGATTTTAATAGTACATCATCGTCTACGGGTGGGTGGGGGTAGCGTT	240		
Db	1335	GCTGATTTTAATAGTAAATAATCATCGTCTACGGGTGGGTGGGGGTAGCGTT	1394		
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Db	1395	AGTAGTGAGTGGGACACACACTTGTGTGTAGAGTATGTTGTGTATATAGTATTA	1454		
QY	301	CTATTACACATTAAAGGCTCCACACAGAAACATTGTATATGGTGTGCTGTAA	357		
Db	1455	CTGTTACACATTAAAGTCTCCACACAGAAACATTGTATATGGTGTGCTGTGCTTAA	1511		

RESULT 11				
LOCUS	E59891			
DEFINITION	Rhicomania-resisting plant.	739 bp	DNA	linear
ACCESSION	E59891			
VERSION	E59891.1	GI:18622727		
KEYWORDS	JP 2000312540-A/3.			
SOURCE	Beet necrotic yellow vein virus.			
ORGANISM	Beet necrotic yellow vein virus			
REFERENCE	viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.			
AUTHORS	1 (bases 1 to 739)			
TITLE	Nomura,S., Kamitani,G., Salto,M., Kiguchi,T., Kusu,S. and Some,C.			
JOURNAL	Rhicomania-resisting plant			
COMMENT	Patent: JP 2000312540-A/3 14-NOV-2000;			
	GENICHI KAMITANI,SHADANHOIN HOKKAIDO TENSAI KYOKAI			
	OS Beet Necrotic yellow vein virus			
	PN JP 2000312540-A/3			
	PD 14-NOV-2000			
	PE 28-APR-1999 JP 1999122628			
	PR SHINJI NOMURA,GENICHI KAMITANI,MINAKO SATO,TADAHIKO KIGUCHI,			
	PI PI SHUNZO KUSUME,			
	PI CHIHIRO SOMA,			
	PC A01H5/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC			
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	mutation			
	location/Qualifiers			
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	/db_xref="taxon:31721"			
BASE COUNT	182 a 117 c 187 g 253 t			
ORIGIN				

Query Match	Similarity	88.3%	Score 315.4	DB 6	Length 739
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Matches 331	Conservative	0	Mismatches 26	Indels	Gaps
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Db	1	ATGTCTAGGGAATAATACCGCTCGACCCATATAAGAAATGTCCTATTGTTGGTGGTGGT	60		
Qy	61	GTTGTGGCTTTCTTTTGTATGCTGGCGTTCAATGACCAACAGCACTGCGACATCTTGGG	120		
Db	61	GTTGTGGCTTTCTTTTGTATGCTGGCGTTCAATGACCAACCAATATAGACACATCTTGGG	120		
Qy	121	GGGTATTACGAGATGCCAACATTTTCTAAAGGTGTATATATAGAGAGCGGTACAAAGATCA	180		
Db	121	GGGTATTACGAGATGCCAACATTTTCTAAAGGTGTATATATAGAGAGCGGTACAAAGATCA	180		
Qy	181	GGCGATTTTAATATTAACAATCATGTCGTTCAGGTCGGGTGGGTGGGTGGGTAGAGCTT	240		
Db	181	GGCGATTTTAATATTAACAATCATGTCGTTCAGGTCGGGTGGGTGGGTGGGTAGAGCTT	240		
Qy	241	AGTAGTCGAGTGGGGCAGCAACTTATTTGTTAGCTATTGTTTCTGTGTTAAATAGTCTCA	300		
Db	241	AGTAGTCGAGTGGGGCAGCAACTTATTTGTTAGCTATTGTTTCTGTGTTAAATAGTCTCA	300		
Qy	301	CTATTACACGATTAAAGGTCTCCACCAGAACACATTTGTAATGTCGTTGGGTTAA	357		
Db	301	CTGTACACGATTAAAGATCTCCACCAGAACATTTGTAATGTCGTTGGGTTAA	357		
RESULT 12					
AF061869					
LOCUS	AF061869	4616 bp	RNA	linear	VRL 26-MAR-2002
DEFINITION	Beet soil-borne mosaic virus RNA2, complete genome.				
ACCESSION	AF061869				
VERSION	AF061869.1	GI:3136264			
KEYWORDS					
SOURCE	beet soil-borne mosaic virus.				
ORGANISM	beet soil-borne mosaic virus				
REFERENCE	1 (bases 1 to 4616)				

AUTHORS Lee, L., Telford, E.B., Batten, J.S., Scholtzof, K.B. and Rush, C.M.
 TITLE Complete nucleotide sequence and genome organization of Beet
 JOURNAL 21670014
 MEDLINE 21670014
 PUBMED 11811691
 REFERENCE 2 (bases 1 to 4616)
 AUTHORS Batten, J.S., Rush, C.M. and Scholtzof, K.-B.G.
 TITLE Direct Submission
 JOURNAL Submitted (28-APR-1998) Plant Pathology and Microbiology, Texas A&M
 University, 120 Peterson Building, College Station, TX 77843-2132,
 USA

FEATURES
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 Location/Qualifiers
 1. 4616
 /organism="beet soil-borne mosaic virus"
 /strain="EA"
 /db_xref="taxon:76343"
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 /translation="MSREITRANKNVPIVGVGVVAFVLLAFMOOKHKHSGDVG
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 4039..4401
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 /translation="MEKSNISIGVYVVKDPIITNDCRLEFSYKGMCLFTNHVETRYGKN
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 RGVFDSCAQODELDNNVY"

CDS
 polyA_site
 BASE COUNT 1124 a 779 c 1220 g 1493 t
 ORIGIN

Query Match 58.3% Score 208.2; DB 14; Length 4616;
 Best Local Similarity 73.9% Pred. No. 6.8e-51;
 Matches 264; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1 ATGTCTAGGGAATTAACCGCTCGACCCCAATTAAGATGTCCTATTGTTGGTGTGTTGT 60
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 Db 3273 ATGTCTAGGGAATTAACCGCTCGACCCCAATTAAGATGTCCTATTGTTGGTGTGTTGT 3332

QY 61 GTTGTGCTTCTTCTTATGATGCTGCGCTTCATGACGAAGACGCGACACATTCCTGGG 120
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 Db 3333 GTTGTGCTTCTTCTTATGATGCTGCGCTTCATGACGAAGACGCGACACATTCCTGGT 3392

QY 121 GGTGATTACGAGATCCCAACATTTTCTAACCGTGTATATATAGACGATTAAGATCA 180
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 Db 3393 GGTGATTACGAGATCCCAACATTTTCTAACCGTGTATATATAGACGATTAAGATCA 3452

QY 181 GGTGATTATTAATGATTAACATCATGCTGCTTACGAGGTCGCTGGGTGCGGAGTACGCTT 240
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 Db 3453 GGTGATTATTAATGATTAACATCATGCTGCTTACGAGGTCGCTGGGTGCGGAGTACGCTT 3512

QY 241 AGTAGTCGAGTGGGCGCAACTATGTTGTTAGCTATGTTTCTGTTTAAATAGTCA 300
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 Db 3513 ACTGCGAAGTGGGCGCAACTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3572

QY 301 CTATTACACGATTAAGTCTCCACAGAACACATTTGTAATGTTGTTGTTGTTGTTAA 357
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 Db 3573 CTATTACGATTAAGTCTCCACAGAACACATTTGTAATGTTGTTGTTGTTGTTGTTAA 3629

RESULT 13
 LRVABCD LRVABCD 3065 bp RNA linear VRL 06-DEC-1995
 LOCUS LRVABCD
 DEFINITION Lymphis ringspot virus RNA for beta-A, beta-B, beta-C, beta-D
 accession 246351.1 GI:1107714
 VERSION 246351.1
 KEYWORDS coat protein.
 ORGANISM Lymphis ringspot virus.
 Lymphis ringspot virus.
 Viruses: ssRNA positive-strand viruses, no DNA stage: Hordeivirus.
 REFERENCE 1 (bases 1 to 3065)
 AUTHORS Solovay, A.G.
 JOURNAL Unpublished

REMARK	2	(bases 1 to 3065)
AUTHORS	Solov'yev A.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-OCT-1994)	Solov'yev A., Institute of Biochemistry and Plant Virology, Messweg 11/12, Braunschweig, Germany
FEATURES	Location/Qualifiers	
source	1. 3065	/organism="Lychnis ringspot virus"
	/db_xref="taxon:44421"	
misc_feature	1. 3065	/note="genomic RNA beta, partial sequence"
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CDS	/citation=[1]	
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	AMANILAIRMGDOPFLSRDDELSTRRPPTGNGQSNALVARDVQPLRDSALHFY	
	DKDIVTSDDPVPDRSRSEAKFQLNWVARAPGNA"	
CDS	850..2211	/function="virus cell-to-cell movement protein"
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	ACSEKERIAAKSFELHSLRPNVDGFIYSGVAGSGSKTIRKLCEADAMCVLANP	
	RLEKETDGQSKTFELCOVLISIVPMISDVIIVDEYILASAEHLIDQRLQATFLIV	
	GVAGNAGDPTASLEIYLPFVYISKTSIRGLKHEMLCKKKGAAPEGPSDEDEIL	
	VADYLGADPTTEKRIATFKETVEDIRAGVNASIYLTECKQEVESYTLFRESDEAM	
	ADSHLRVALTRHKKLITRAEPGVSSFLNGELKTSADSRKTESKSYADSSSA	
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CDS	2180..2551	/function="virus cell-to-cell movement protein"
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	/db_xref="SPTREMBL:O83078"	
	/translation="MPTVOAQRPKKYMPIVVGVLIGLFAVLIPTNOKHATQSGDNTHI	
	KFNAGSGYDQGNKRINYNKNNNLAPKYGKGLSNASSVDMLGICIAIAGIYGEYLR	
	KRRHDECTGCPDCKICGMR"	
CDS	2406..2879	/function="virus cell-to-cell movement protein"
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	/protein_id="CAAB6472.1"	
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	/db_xref="SPTREMBL:O83079"	
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	DPEVIRKIHIFQNPYGRTPGIGIMDWITGLVYFWPRLIYLGIIIEFIWEKNI"	
BASE COUNT	889 a 597 c 681 g 898 t	
ORIGIN		
Query Match	18.3%, Score 65.4; DB 14; Length 3065;	
Best Local Similarity	59.9%; Pred. No. 1.9e-08;	
Matches 130; Conservative	0; Mismatches 81; Indels 6; Gaps 1;	
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2180	ATGCCGACTCAATGAGCCAGGCGCCCAATAGTATGATGTTGTTGTTGGCT 2239	

Qy	61	GTGTGGCTTCTTTTGTATGTCGGCGTTATGACGACAGCAGCTGCGACATTTGGG	120
Db	2240	TTGATAGGTCTTTTGGTATCTGATCTTATACCAATCAAAAGCAGCAGCATCAGGT	2299
Qy	121	GGTATATACGAGTCCCAACATTTTTCACGSGTGATATATACGACGGTCAAGATCA	180
Db	2300	GATATATA-----TTCACAAATTTTGGCCACGCGTGCTTATATCAAGACGGTAATMAAGA	2353
Qy	181	GCTGATTTTATAGTACCAATCATCGTTCCTTACGGGT	217
Db	2354	ATAATTTATACCAAAATAATTAATTTAGCTTACGGTT	2390
RESULT 14			
LOCUS	BSBV3GNS		
DEFINITION	Beet soil-borne virus genes for 13k, 22k and 48k proteins.		
ACCESSION	266493		
VERSION	266493.2	GI:11595427	
KEYWORDS	13k protein; 22k protein; 48k protein.		
SOURCE	Beet soil-borne virus.		
ORGANISM	Beet soil-borne virus		
REFERENCE	1. (bases 1 to 3005)		
AUTHORS	Koenig R., Beier, C., Commandeur, U., Luth, U., Kaufmann, A. and Lüddecke, P.		
TITLE	Beet soil-borne virus, RNA 3--a further example of the heterogeneity of the gene content of furovirus genomes and of triple gene block-carrying RNAs		
JOURNAL	Virology 216 (1), 202-207 (1996)		
MEDLINE	96187804		
PUBMED	8614988		
REFERENCE	2. (bases 1 to 3005)		
AUTHORS	Koenig, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-OCT-1995) Koenig R., Biologische Bundesanstalt fuer Land- und Forstwirtschaft, Institut fuer Biochemie/Pflanzenvirologie, Messegew 11, Braunschweig, Germany, D38104		
REMARK	3. (bases 1 to 3005)		
REFERENCE	Koenig, R.		
AUTHORS	Direct Submission		
TITLE	Submitted (04-DEC-2000) Koenig R., Biologische Bundesanstalt fuer Land- und Forstwirtschaft, Institut fuer Biochemie/Pflanzenvirologie, Messegew 11, Braunschweig, Germany, D38104		
JOURNAL	On Dec 6, 2000 this sequence version replaced gi:1225930.		
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FEATURES			
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	1..3005		
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	405..1688		
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5'UTR			
CDS			

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	/citation=[1]
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	/db_xref="GI:1225932"
	/db_xref="SPTREMBL:O65728"
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BASE COUNT 917 a 507 c 664 g 917 t

ORIGIN

Query Match 16.7%; Score 59.6; DB 14;

Best Local Similarity 59.1%; Pred. No. 9.9e-07;

Matches 123; Conservative 0; Mismatches 79; Indels 6; Gaps 1;

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Oy.   5 CTAGCGAATAACCCCTGCAGCCCATTAAGAATGTCCATTGTGTGTGTTG 64
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Db    1665 CTAAAGACATCGGCCCGCAGACTTAAATGAATGTTCGCAATAGTCGTATTTGCA 1744
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Oy.   65 TGGCTTCTTGTTATTTGGTGGGCTTCAGCAGCAAGCGTGGCACATCTGGGGTG 124
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Db    1745 TTGCATTGTTCAGTTTTTAACTATTAACAATCAGAACACGCCACAGTCGGAGATTA 1804
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Oy    125 ATTACGAGATCCCAACATTTTCTAACGGTGTATATATAGAGCGGTACAGATCAGCTG 184
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Db    1805 ATA-----TTCACACAA GTTTTCTAACGGTGTGAAAATTTCAGACGGCAATAAGCGTGTTC 1858
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Oy    185 ATTTATATGTAACAATCATCGTGCTTA 212
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Db    1859 ATTATATTAAGATATATCTTAGAGCTTA 1886
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RESULT 15

SZSZBTACD

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

psrBETACD 3591 bp ss-RNA linear VRL_02-AUG-1996

Poa semilient virus beta genomic segment beta-A, beta-B, beta-C

M81486

M81486.1 GI:1478094

Poa semilient virus cDNA to genomic RNA.

Poa semilient virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.

1 (bases 1 to 3591)

Agranovsky,A.A., Karasev,A.V., Novikov,V.K., Lunina,N.A., Logunov,S. and Tyulkina,L.G.

Poa semilient virus, a hordeivirus having no internal polydispersed poly(A) in the 3' non-coding region of the RNA genome

J. Gen. Virol. 73 (Pt 8), 2085-2092 (1992)

JOURNAL MEDLINE 92356087

PUBMED 1645144

REFERENCE 2 (bases 1 to 3591)

FEATURES	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	COMMENT	FEATURES
JOURNAL MEDLINE PUBMED	96204567 8623558	Collopy, A. G., Savenkov, E. I., Agrimovsky, A. A. and Morozov, S. Y.	Comparisons of the genomic cis-elements and coding regions in RNA beta components of the hordeivirus barley stripe mosaic virus, lynchis ringspot virus, and poa semilient virus	Virology 219 (1), 9-18 (1996)			
REFERENCE	3 (bases 1 to 3591)	Solovay, A.	Direct Submission	Submitted (13-AUG-1993)	Andrey G. Solovay, Institute of Biochemistry and Plant Virology, Braunschweig, D-38104, Germany	On Aug 2, 1996 this sequence version replaced gi:333326.	
COMMENT	Location/Qualifiers						
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CDS		/function="virus cell-to-cell movement protein"	/codon_start=1	/product="beta-B protein"	/protein_id="AAB0577.1"	/db_xref="GI:1478096"	
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CDS		/translation="MPAKTTSVGSRPKNPYIVAGIGVGLFAVLIIRANOKHSHESDDNIHFFANGSGYRDSKCIYHRNNPFAVGNASPGMLPTLTITIGIVSLMATRGELT MCGNSPLIGHMCEGCAECYRCGLDRDLPPNSV"	2773..3261				
CDS		/function="virus cell-to-cell movement protein"	/codon_start=1	/product="beta-C protein"	/protein_id="AAB0579.1"	/db_xref="GI:1478098"	
CDS		/translation="MAMPHLGCGSCPLCSQSSSEFPYICPEERLMEETPPSATTVE RNAEENFVAMIDRNLYLTLCISLALSVSLAYITFSGNNPPYGVGYFVODLMSVEV RFEGHPADPKVIASIIHNMOKNPFQVSPLEMBGLNVLVSLVSLKLFYVGLFLLLIIIT FK"					
BASE COUNT	1049 a	718 c	842 g	982 t			
ORIGIN							
Query Match	14.88:	Score 53;	DB 14:	Length 3591;			
Best Local Similarity	58.58:	Pred. No. 9.1e-05;					
Matches 114;	Conservative 0;	Mismatches 75;	Indels 6;	Gaps 1;			
21	TCGACCCAAATGAAGATGCGCTATGTTGCGGCTTGTGTGTCGCTTCTTGTGATT	80					

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Db 2588 TAGACCTAATAGATATGGCAATTGTAGTGTATAGGTAGTAGTTTATTTCCTTA 2647
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Db 2648 CTTAATTCTTTCCTAATCAGAAACATTCTAGTCTGAGATTAATA-----TCCACAA 2701
QY 141 ATTTCTAACGGTGTATATATAGACGTACAGATCAGCTGATTTTATATAGTAACAA 200
Db 2702 ATTTGCCAAGCGTGGAGATATCGAGACGGTCTAAGTGTATTCTTACCATCGAACA 2761
QY 201 TCATCGTCTTACGG 215
Db 2762 CCCTTCGCCCTATGG 2776

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Search completed: March 12, 2003, 09:31:48
 Job time : 1177 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 14:24:19 : Search time 175 Seconds
(without alignments)
4594.077 Million cell updates/sec

Title: US-09-936-011-3

Perfect score: 357
Sequence: 1 atgtctagggaataacgcg.....gttaatgctgtgtgttaa 357

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	347.4	97.3	357	21	AAA75877
3	328.2	91.9	357	22	AAZ26890
4	328.2	91.9	4608	22	AAZ26889
5	315.4	88.3	739	22	AAZ26891
6	50.6	14.2	507	24	ABK86954
7	42.6	11.9	507	24	ABK86955
8	36.8	10.3	1230025	20	AAZ91990
9	36.6	10.3	4039	22	AAH34822

10	36.6	10.3	4039	24	ABL90346	Human polynucleoti
11	36.6	10.3	4040	21	AAZ77977	Human cancer assoc
12	36.6	10.3	5544	24	ABL61761	Colon adenocarcino
13	36.6	10.3	5549	23	AAZ87055	DNA encoding novel
14	36.4	10.2	2215	24	AB199688	Mouse ischaemic co
15	35.6	10.0	1668	24	ABK40083	Human chemically p
16	35.2	9.9	14920	24	ABN80146	Human chemically m
17	34.8	9.7	2231	19	AAZ32556	Candida albicans C
18	34.8	9.7	3243	19	AAZ32555	Candida albicans C
19	34.8	9.7	3243	19	AAZ32555	Candida albicans C
20	34.6	9.7	2772	23	ABL25868	DNA encoding novel
21	34.2	9.6	493	22	ABZ58243	Human foetal liver
22	34.2	9.6	493	22	ABA27397	Probe #5863 for ge
23	34.2	9.6	493	22	AAK06331	Human brain expres
24	34.2	9.6	493	22	AAK31999	Human bone marrow
25	34.2	9.6	493	22	AAK31999	Probe #546 used t
26	34.2	9.6	493	24	ABZ06764	Human genome-deriv
27	34.2	9.6	2328	23	ABZ06764	DNA encoding novel
28	34.2	9.6	2494	24	ABK31539	Signal transductio
29	34.2	9.6	5296	22	AAZ77661	Human immune/hema
30	34.2	9.6	47670	23	ABL16824	Human immune/hema
31	34.2	9.6	50368	23	ABL16768	Drosophila melanog
32	33.8	9.5	406	24	ABN75893	Human ORE840 CDNA,
33	33.8	9.5	1794	23	AAZ8187	DNA encoding novel
34	33.8	9.5	3598	22	AAH18642	Human CDNA sequenc
35	33.2	9.3	5971	23	AAH32383	Human immune syste
36	32.8	9.2	2361	23	AAZ54928	Staphylococcus aur
37	32.6	9.1	5986	24	AAZ61433	Human gene regulat
38	32.6	9.1	5986	24	ABK31499	Signal transductio
39	32.6	9.1	6681	24	ABZ54303	Chemically treated
40	32.6	9.1	6681	24	ABZ54303	Human immune syste
41	32.4	9.1	2527	15	AAZ56756	Chitinase 1 gene.
42	32.4	9.1	7434	24	AAZ28386	Human chemically t
43	32.4	9.1	29376	23	ABZ08834	Drosophila melanog
44	32.4	9.1	107602	24	AAZ96657	DNA of the PAC clo
45	32.4	9.1	107612	24	ABL54503	Human PAC clone se

ALIGNMENTS

RESULT 1	AAA75878	standard: DNA; 357 BP.
ID	AAA75878	
AC	AAA75878;	
DT	22-JAN-2001	(first entry)
DE	DNA encoding a P13 variant of Beet necrotic yellow vein mosaic virus.	
KW	P13 protein; triple gene block 2; TGB2; resistance; group I virus; ss.	
OS	Beet necrotic yellow vein mosaic virus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..357
FT		/*tag= a
FT		/product= "P13 protein"
XX		
PN	WO200055301-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	07-MAR-2000; 2000WO-EP02176.	
PR	12-MAR-1999; 99EP-0200773.	
XX		
PA	(CNRS) CNRS CENT NAT RECH SCI.	
XX		
PI	Jonard G, Lauber E, Gullley H, Richards K;	
XX		
DR	WPI; 2000-602114/57.	

DR P-PSDB; AAB18802.

XX Inducing viral resistance into a plant or a plant cell, especially beet
 PT necrotic yellow vein virus-resistance into a sugar beet plant or cell
 PT by transforming the plant cell with triple gene block of the virus

XX PS Disclosure; Fig 2; 27pp; English.

CC The present sequence encodes a P13 protein variant of Beet necrotic
 CC yellow vein mosaic virus. The P13 sequence is a triple gene block 2
 CC (TGB2) sequence. It is used for inducing resistance to a group I virus.
 CC The method is useful for inducing resistance to a plant cell or plants
 CC such as sugar beet, potato, barley or peanut against group I virus
 CC such as hordeoviruses, benyviruses, pecluviruses and pomoviruses,
 CC preferably barley stripe mosaic virus, potato mop top virus, peanut
 CC clump virus and the beet soil-borne virus, more preferably beet
 CC necrotic yellow vein virus (BNYVV).

SQ Sequence 357 BP; 84 A; 60 C; 96 G; 117 T; 0 other;

Query Match 100.0%; Score 357; DB 21; Length 357;

Best Local Similarity 100.0%; Pred. No. 5.7e-101; Mismatches 0; Indels 0; Gaps 0;

Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGCTGCTATGTTGTTGTTGT 60
 DB 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGCTGCTATGTTGTTGTTGT 60
 QY 61 GTTGGGCTTTCTTTGTTATGCTGCGCTTCATGACAGACAGCTGCGACACATTCGGG 120
 DB 61 GTTGGGCTTTCTTTGTTATGCTGCGCTTCATGACAGACAGCTGCGACACATTCGGG 120
 QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGAGCGTCAACATCA 180
 DB 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGAGCGTCAACATCA 180
 QY 181 GGTGATTATATAGTAAATCATGCTGCTTACGGGTGCGGTGCGGTGCGGTACGCTT 240
 DB 181 GGTGATTATATAGTAAATCATGCTGCTTACGGGTGCGGTGCGGTGCGGTACGCTT 240
 QY 241 AGTAGTCGAGTGGGAGCAACTTATGCTTACGCTTATGCTTATATAGTCA 300
 DB 241 AGTAGTCGAGTGGGAGCAACTTATGCTTACGCTTATGCTTATATAGTCA 300
 QY 301 CTATTACAAAGATTAAAGTCTCCACAGACACATTTGTAATGCTGTGTTAA 357
 DB 301 CTATTACAAAGATTAAAGTCTCCACAGACACATTTGTAATGCTGTGTTAA 357

RESULT 2
 AAA75877 standard; DNA: 357 BP.

AC AAA75877;

XX 22-JAN-2001 (first entry)

DE DNA encoding a P13 protein of Beet necrotic yellow vein mosaic virus.

XX P13 protein; triple gene block 2; TGB2; resistance; group I virus; ss.

XX Beet necrotic yellow vein mosaic virus.

XX Key Location/Qualifiers

FT CDS 1..357 /*tag- a

FT WO200053301-A2. /product= "P13 protein"

XX 21-SEP-2000.

XX 07-MAR-2000; 2000WO-EP02176.

XX 12-MAR-1999; 99EP-0200773.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Jonard G, Lauber E, Guillely H, Richards K;

XX WPI: 2000-602114/57.

DR P-PSDB; AAB18801.

XX Inducing viral resistance into a plant or a plant cell, especially beet
 PT necrotic yellow vein virus-resistance into a sugar beet plant or cell
 PT by transforming the plant cell with triple gene block of the virus

XX PS Disclosure; Fig 1; 27pp; English.

CC The present sequence encodes a P13 protein of Beet necrotic yellow
 CC vein mosaic virus. The sequence is a triple gene block 2 (TGB2)
 CC sequence. It is used for inducing resistance to a group I virus. The
 CC method is useful for inducing resistance to a plant cell or plants
 CC such as sugar beet, potato, barley or peanut against group I virus
 CC such as hordeoviruses, benyviruses, pecluviruses and pomoviruses,
 CC preferably barley stripe mosaic virus, potato mop top virus, peanut
 CC clump virus and the beet soil-borne virus, more preferably beet
 CC necrotic yellow vein virus (BNYVV).

SQ Sequence 357 BP; 89 A; 58 C; 93 G; 117 T; 0 other;

Query Match 97.3%; Score 347.4; DB 21; Length 357;

Best Local Similarity 98.3%; Pred. No. 5.5e-98; Mismatches 6; Indels 0; Gaps 0;

Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGCTGCTATGTTGTTGTTGT 60
 DB 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGCTGCTATGTTGTTGTTGT 60
 QY 61 GTTGGGCTTTCTTTGTTATGCTGCGCTTCATGACAGACAGCTGCGACACATTCGGG 120
 DB 61 GTTGGGCTTTCTTTGTTATGCTGCGCTTCATGACAGACAGCTGCGACACATTCGGG 120
 QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGAGCGTCAACATCA 180
 DB 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATATAGAGAGCGTCAACATCA 180
 QY 181 GGTGATTATATAGTAAATCATGCTGCTTACGGGTGCGGTGCGGTGCGGTACGCTT 240
 DB 181 GGTGATTATATAGTAAATCATGCTGCTTACGGGTGCGGTGCGGTGCGGTACGCTT 240
 QY 241 AGTAGTCGAGTGGGAGCAACTTATGCTTACGCTTATGCTTATATAGTCA 300
 DB 241 AGTAGTCGAGTGGGAGCAACTTATGCTTACGCTTATGCTTATATAGTCA 300
 QY 301 CTATTACAAAGATTAAAGTCTCCACAGACACATTTGTAATGCTGTGTTAA 357
 DB 301 CTATTACAAAGATTAAAGTCTCCACAGACACATTTGTAATGCTGTGTTAA 357

RESULT 3
 AAF26890 standard; DNA: 739 BP.

AC AAF26890;

XX 09-APR-2001 (first entry)

DE Beet necrotic yellow vein virus promoter sequence SEQ ID NO:2.

XX Beet necrotic yellow vein virus; BNYVV; transformed plant;

XX Rhizomania disease-resistant plant; promoter; ds.

XX Beet necrotic yellow vein mosaic virus.

XX JP2000312540-A.


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XX 14-NOV-2000.
PD 28-APR-1999; 99JP-0122628.
XX 28-APR-1999; 99JP-0122628.
XX 28-APR-1999; 99JP-0122628.
XX (HOKK-) HOKKAIDO PREFECTURE.
XX (HOKK-) HOKKAIDO TENSAN KYOKAI SH.
XX WPI: 2001-054202/07.
XX A Rhizomania disease-resistant plant -
XX Claim 14; Page 9; 11pp; Japanese.
XX The present invention describes a method for producing a transformed
XX plant in which resistance against beet necrotic yellow vein virus
XX (BNYV) is given by transforming expressably a gene derived from BNYV
XX genome or a DNA corresponding to its part or a DNA substantially same
XX as it in a plant genome. The vector structure can be used for
XX transforming a plant or a plant cell having BNYV resistance. The
XX present sequence represents a wild type BNYV promoter nucleotide
XX sequence for use in the method of the invention.
XX
SQ Sequence 739 BP; 184 A; 114 C; 189 G; 252 T; 0 other;
Query Match 91.9%; Score 328.2; DB 22; Length 739;
Best Local Similarity 95.0%; Pred. No. 6.9e-92;
Matches 339; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGTCCTATTGTTGGTGTGTTGT 60
DB 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGTCCTATTGTTGGTGTGTTGT 60
QY 61 GTTGTGGCTTTCTTTGTAATGCTGCGCTTCATGCAAGACAGCTGCGACATCTCTGG 120
DB 61 GTTGTGGCTTTCTTTGTAATGCTGCGCTTCATGCAAGACAGCTGCGACATCTCTGG 120
QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATAGAGAGGTACAAGATCA 180
DB 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATAGAGAGGTACAAGATCA 180
QY 181 GCTGATTTTAAATAGTAACATCATCTGCTTAACGGTGTGCTGCGGTACGCTT 240
DB 181 GCTGATTTTAAATAGTAACATCATCTGCTTAACGGTGTGCTGCGGTACGCTT 240
QY 241 AGTAGTCGAGTGGGACGACCACTTGTGTTAGCTATTGTCGTGTTAATAGATCA 300
DB 241 AGTAGTCGAGTGGGACGACCACTTGTGTTAGCTATTGTCGTGTTAATAGATCA 300
QY 301 CTATTACAGGATTAAAGTCTCCACAGACACATTTGTAATGTCGCTTGGTTAA 357
DB 301 CTATTACAGGATTAAAGTCTCCACAGACACATTTGTAATGTCGCTTGGTTAA 357
RESULT 4
AAF26889
ID AAF26889 standard; DNA: 4609 BP.
XX AAF26889;
XX
XX 09-APR-2001 (first entry)
XX Beet necrotic yellow vein virus RNA-2 nucleotide sequence SEQ ID NO:1.
XX Beet necrotic yellow vein virus; BNYV; transformed plant;
XX Rhizomania disease-resistant plant; ds.
XX Beet necrotic yellow vein mosaic virus.
XX JP2000312540-A.

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PD 14-NOV-2000.
XX 28-APR-1999; 99JP-0122628.
XX 28-APR-1999; 99JP-0122628.
XX 28-APR-1999; 99JP-0122628.
XX (HOKK-) HOKKAIDO PREFECTURE.
XX (HOKK-) HOKKAIDO TENSAN KYOKAI SH.
XX WPI: 2001-054202/07.
XX A Rhizomania disease-resistant plant -
XX Claim 13; Page 7-9; 11pp; Japanese.
XX The present invention describes a method for producing a transformed
XX plant in which resistance against beet necrotic yellow vein virus
XX (BNYV) is given by transforming expressably a gene derived from BNYV
XX genome or a DNA corresponding to its part or a DNA substantially same
XX as it in a plant genome. The vector structure can be used for
XX transforming a plant or a plant cell having BNYV resistance. The
XX present sequence represents a specifically claimed BNYV nucleotide
XX sequence for use in the method of the invention.
XX
SQ Sequence 4609 BP; 1187 A; 765 C; 1221 G; 1436 T; 0 other;
Query Match 91.9%; Score 328.2; DB 22; Length 4609;
Best Local Similarity 95.0%; Pred. No. 1.4e-91;
Matches 339; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGTCCTATTGTTGGTGTGTTGT 60
DB 3284 ATGCTAGGGAATTAACCGCTCGACCAATAGAAATGTCCTATTGTTGGTGTGTTGT 3343
QY 61 GTTGTGGCTTTCTTTGTAATGCTGCGCTTCATGCAAGACAGCTGCGACATCTCTGG 120
DB 3344 GTTGTGGCTTTCTTTGTAATGCTGCGCTTCATGCAAGACAGCTGCGACATCTCTGG 3403
QY 121 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATAGAGAGGTACAAGATCA 180
DB 3404 GGTGATTACGAGTCCCAACATTTCTTAACGGTGTATATAGAGAGGTACAAGATCA 3463
QY 181 GCTGATTTTAAATAGTAACATCATCTGCTTAACGGTGTGCTGCGGTACGCTT 240
DB 3464 GCTGATTTTAAATAGTAACATCATCTGCTTAACGGTGTGCTGCGGTACGCTT 3523
QY 241 AGTAGTCGAGTGGGACGACCACTTGTGTTAGCTATTGTCGTGTTAATAGATCA 300
DB 3524 AGTAGTCGAGTGGGACGACCACTTGTGTTAGCTATTGTCGTGTTAATAGATCA 3583
QY 301 CTATTACAGGATTAAAGTCTCCACAGACACATTTGTAATGTCGCTTGGTTAA 357
DB 3584 CTATTACAGGATTAAAGTCTCCACAGACACATTTGTAATGTCGCTTGGTTAA 3640
RESULT 5
AAF26891
ID AAF26891 standard; DNA: 739 BP.
XX AAF26891;
XX
XX 09-APR-2001 (first entry)
XX Beet necrotic yellow vein virus mutant promoter sequence SEQ ID NO:3.
XX Beet necrotic yellow vein virus; BNYV; transformed plant;
XX Rhizomania disease-resistant plant; promoter; ds.
XX Beet necrotic yellow vein mosaic virus.
XX Synthetic.
XX JP2000312540-A.

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PD 14-NOV-2000.
 XX 28-APR-1999; 99JP-0122628.
 XX 28-APR-1999; 99JP-0122628.
 XX (HOKK-) HOKKAIDO PREFECTURE.
 PA (HOKK-) HOKKAIDO TENSAN KYOKAI SH.
 XX WPI; 2001-054202/07.
 XX A Rhizomania disease-resistant plant -
 XX Claim 15; Page 9; 11pp; Japanese.
 CC The present invention describes a method for producing a transformed
 CC plant in which resistance against beet necrotic yellow vein virus
 CC (BNYVV) is given by transforming expressably a gene derived from BNYVV
 CC genome or a DNA corresponding to its part or a DNA substantially same
 CC as it in a plant genome. The vector structure can be used for
 CC transforming a plant or a plant cell having BNYVV resistance. The
 CC present sequence represents a mutant BNYVV promoter nucleotide
 CC sequence for use in the method of the invention.

Sequence 739 BP; 182 A; 117 C; 187 G; 253 T; 0 other;

Query Match 88.3%; Score 315.4; DB 22; Length 739;
 Best Local Similarity 92.7%; Pred. No. 6.5e-88;
 Matches 331; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 1 ATGTCTGGGAATTAACCGCTGACCAATAGAAATGTCCTATTGTTGGTGTGT 60
 Db 1 ATGTCTGGGAATTAACCGCTGACCAATAGAAATGTCCTATTGTTGGTGTGT 60
 OY 61 GTTGTGCTTTCTTTGTTATGCTGCTGCTGATGACGACGACCTGACACATTTG 120
 Db 61 GTTGTGCTTTCTTTGTTATGCTGCTGCTGATGACGACGACCTGACACATTTG 120
 OY 121 GGTGATTACGGAGTCCCAACATTTCTAAGCTGATATATAGACGATACAGATCA 180
 Db 121 GGTGATTACGGAGTCCCAACATTTCTAAGCTGATATATAGACGATACAGATCA 180
 OY 181 GCTGATTTTAAATAGTAACATCATGCTGCTTACGGGCTGGGCTGCTGGGCT 240
 Db 181 GCTGATTTTAAATAGTAACATCATGCTGCTTACGGGCTGGGCTGCTGGGCT 240
 OY 241 AGTAGTGAAGTGGGACCACTTATGTTAGCTATGTTCTGTGTAATAGTGTCA 300
 Db 241 AGTAGTGAAGTGGGACCACTTATGTTAGCTATGTTCTGTGTAATAGTGTCA 300
 OY 301 CTAATTACAGATTAAGGCTCCACGACCAATTTGTAATGCTGCTGTTAA 357
 Db 301 CTAATTACAGATTAAGGCTCCACGACCAATTTGTAATGCTGCTGTTAA 357

RESULT 6
 ABRK6954
 ID ABRK6954 standard; cDNA; 507 BP.

ABR6954;

24-SEP-2002 (first entry)

Potato mop-top virus (PMTV) triple-gene-block (TGB)-2 cDNA.

XX Potato; antiviral; triple-gene-block 2; TGB-2; PMTV;
 XX Potato mop-top virus; Pomovirus; spiraling; dwarfing; mopping;
 XX chlorotic chevron; necrotic chevron; blotching; tuber cracking;
 KM necrotic conchoidal layer; viral movement; transgenic; molecular marker;
 KM resistance; agriculture; gene; ss.

XX Potato mop-top virus.
 OS

Key Location/Qualifiers
 CDS 37..396
 FT /*tag= a
 FT /product= "TGB-2"

W0200250281-A1.

27-JUN-2002.

18-DEC-2001; 2001WO-SE02805.

21-DEC-2000; 2000SE-0004755.

(PLAN-) PLANT SCI SWEDEN AB.

Melander M, Lee M;

WPI; 2002-508804/54.

P-PSDB; MAU79576.

Nucleic acid molecule for producing plants with increased resistance against infection by potato mop-top virus comprises a structural gene encoding a triple-gene-block 2 polypeptide from the virus -

Disclosure; Page 31; 36pp; English.

The invention discloses a nucleic acid molecule comprising a promoter operably linked to a structural gene encoding a triple-gene-block 2 (TGB-2) polypeptide from potato mop-top virus (PMTV) which differs from the wild-type polypeptide at a number of residues. The potato crop (Solanum tuberosum) is susceptible to PMTV which belongs to the genus Pomovirus. The main symptoms of the disease are spiraling, dwarfing (mopping), chlorotic and necrotic chevrons, blotching and tuber cracking and necrotic conchoidal layers. PMTV has a tripartite RNA genome, of which RNA 2 encodes for four proteins in a triple-gene-block and all three seem to be responsible for long-distance viral movement within the plant. The mutant TGB-2 is useful for producing transgenic plants, in particular, the potato plant, with an increased resistance against infection by PMTV. Portions of the mutant TGB-2 are useful as molecular markers for detecting a transgenic plant and for detecting a food product from the transgenic plant. The advantage the mutant TGB-2 brings is that it is able to render potato plants resistant by using solely a single gene which is easy to follow and maintain during a breeding program. The transgenic plants can be grown even in fields infected by PMTV, which increases the economic value of the yield obtained from such an infected field. The sequence presented is the wild-type TGB-2 cDNA from PMTV.

Sequence 507 BP; 143 A; 94 C; 106 G; 164 T; 0 other;

Query Match 14.2%; Score 50.6; DB 24; Length 507;
 Best Local Similarity 56.5%; Pred. No. 1.1e-05;
 Matches 117; Conservative 0; Mismatches 84; Indels 6; Gaps 1;

OY 6 TAGGGAATTAACCGCTGACCAATAGAAATGTCCTATTGTTGGTGTGTGT 65
 Db 48 TAACGAATTTGAGCGCGACCAATATATATGTCGCGGTATGTCAGATGTCAT 107
 OY 66 GCGTTCTTTGTTATGCTGCGCTTCATGACGACGAGCTGCGACATCTGGGGTGA 125
 Db 108 TTGCTTTTGGGTTTTTAACAGTTACCAATCAAAACACGCTACTCATGAGGTAA 167
 OY 126 TTACGAGTCCCAACATTTTCTAAGCTGTTATATAGAGAGCGGTACAAGATCAGCTGA 185
 Db 168 TA-----TACATTAATTTTCTTAACGCTGCGCTGTACAGGAGCGTCTAAGAGTATTA 221
 OY 186 TTTTATAGTAACATCATGCTGCTTA 212
 Db 222 GTATTAATTTAATTAATCCAGAGCTTA 248

RESULT 7
 ABRK6955
 ID ABRK6955 standard; cDNA; 507 BP.

XX	ABK68955;
AC	
XX	24-SEP-2002 (first entry)
DT	
XX	Mutant potato mop-top virus (PMTV) triple-gene-block (TGB)-2 cDNA.
DE	
XX	Potato; antiviral; triple-gene-block 2; TGB-2; PMTV; 13kDnmt;
KW	chlorotic chevron; necrotic chevrons; blotching; tuber cracking;
KM	necrotic conchoidal layer; viral movement; transgenic; molecular marker
XX	resistance; agriculture; gene; ss; mutant.
OS	Potato mop-top virus.
XX	Synthetic.
FH	
XX	Key
CD	Location/Qualifiers
FT	37..396
FT	/tag= a
FT	/product= "TGB-2 mutant (13kDnmt)"
FT	/replace(188,g)
FT	/tag= b
FT	/replace(191,g)
FT	/tag= c
FT	/replace(193,c)
FT	/tag= d
FT	/replace(194,t)
FT	/tag= e
FT	/replace(195,g)
FT	/tag= f
FT	/replace(197,a)
FT	/tag= g
FT	/replace(204,c)
FT	/tag= h
FT	/replace(206,g)
FT	/tag= i
FT	/replace(208,T)
FT	/tag= j
FN	
PN	WO200250281-A1.
PD	
-	27-JUN-2002.
PF	18-DEC-2001; 2001MO-SEQ02805.
XX	
PR	21-DEC-2000; 2000SE-0004755.
XX	
PA	(PLAN-) PLANT SCI SWEDEN AB.
PI	
DR	Melander M, Lee M:
XX	
DR	WPJ: 2002-508804/54.
XX	P-PDB: AAU79577.
PT	
XX	Nucleic acid molecule for producing plants with increased resistance
PT	against infection by potato mop-top virus comprises a structural gene
PT	encoding a triple-gene-block 2 polypeptide from the virus -
PS	
XX	Example 3; Page 32; 36pp; English.
CC	The invention discloses a nucleic acid molecule comprising a promoter
CC	operably linked to a structural gene encoding a triple-gene-block 2
CC	(TGB-2) polypeptide from potato mop-top virus (PMTV) which differs from
CC	the wild-type polypeptide at a number of residues. The potato crop
CC	(Solanum tuberosum) is susceptible to PMTV which belongs to the genus
CC	Pomovirus. The main symptoms of the disease are spraing, dwarfing
CC	(mopring), chlorotic and necrotic chevrons, blotching and tuber cracking
CC	and necrotic conchoidal layers. PMTV has a tripartite RNA genome, of
CC	which RNA 2 encodes for four proteins in a triple-gene-block and all
CC	three seem to be responsible for long-distance viral movement within the
CC	plant. The mutant TGB-2 is useful for producing transgenic plants, in
CC	particular, the potato plants, with an increased resistance against
CC	infection by PMTV. Portions of the mutant TGB-2 are useful as molecular

	CC	makesfor detecting a transgenic plant and for detecting a food product
	CC	from the transgenic plant. The advantage the mutant rbb-2 brings is that
	CC	it is able to render potato plants resistant by using solely a single
	CC	gene which is easy to follow and maintain during a breeding program. The
	CC	transgenic plants can be grown even in fields infected by PMTV, which
	CC	increases the economic value of the yield obtained from such an infected
	CC	field. The sequence presented is a mutant rbb-2 (13kmut) cDNA from PMTV.
	XX	
SO	Sequence 507 BP; 145 A; 95 C; 104 G; 163 T; 0 other:	
	Query Match	11.9%; Score 42.6; DB 24; Length 507;
	Best Local Similarity	54.1%; Pred. No. 0.0035;
	Matches 112; Conservative	0; Mismatches 89; Indels 6; Gaps 1
OY	6 TAGGCAATTAACCGCTGCAGCCAATAAGANGTGCCTATTGTGGTGTTGGTTCGT	65
Db	48 TAACCAAAATTTGAGCGCAGCCAAATAATATATGCCCGTAGTGTGGCAGTGAAT	107
OY	66 GGCTTCCTTGTATGCGGGGGTTCATGACGACAGCAGTGGACACATTCTGGGGCTGA	125
Db	108 TTGCTCTTTTCGGTTTTTTAACAGTTACCAATCAAAAACGCTACTCAATCAAGTGATTA	167
OY	126 TTACGAGATCCCACATTTTCTAACGGTGTATATATAGAGACGGTACAAGATCACCTGA	185
Db	168 TA-----TACATAAATTTTGGTAAGCGTGGCCAAITTCAGGAGAAGCTGCTAAGATTTAA	221
OY	186 TTTTAAATAGTAACAATCATCTGCTTA	212
Db	222 GTATAATGTATAATATATCCAGAGCTTA	248
RESULT: 8		
AAK91990/c		
ID	AAK91990 standard; DNA; 1230025 BP.	
XX		
AC	AAK91990;	
XX		
DT	13-SEP-1999 (first entry)	
DE		
XX	Nucleotide sequence of the complete genome of Chlamydia pneumoniae.	
KM	Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;	
KW	sinusitis; purulent otitis media; erythema nodosum; pharyngitis;	
XX	vaccine; neutralising epitope; ss.	
OS	Chlamydia pneumoniae.	
PV	WC0927105-A2.	
PN		
XX	03-JUN-1999.	
PD		
XX	20-NOV-1998; 98WO-IB01890.	
PF		
PR	04-NOV-1998; 98US-0107078.	
PR	21-NOV-1997; 97FR-0014673.	
PA	(GEST) GENSET.	
XX		
PI	Griffais R;	
PT		
DR	WP1; 1999-357842/30.	
XX		
PS	Genome sequence of Chlamydia pneumoniae	
XX	Claim 1; Page 291-611; 1912pp; English.	
CC	The present sequence represents the complete genome of Chlamydia	
CC	pneumoniae, and encodes proteins AY34584-Y35879. C. pneumoniae causes	
CC	respiratory disease such as pneumonia and bronchitis and is thought	
CC	to be a contributing factor in heart disease, sarcoidosis, sinusitis,	
CC	purulent otitis media, erythema nodosum or pharyngitis. The polypeptides	
CC	encoded by the open reading frames of the C. pneumoniae genome (see	
CC	AY34584-Y35879) can be used in immunogenic compositions as vaccines.	

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 4039 BP; 1174 A; 790 C; 789 G; 1283 T; 3 other;

Query Match 10.3%; Score 36.6; DB 24; Length 4039;
 Best Local Similarity 49.7%; Pred. No. 0.59;

Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 123 TGTATGCGAGTCCCAACATTTCTACGGTGTATATATAGACGGTACAGATCAGC 182
 DB 585 TGACCCCTGGCAGCAACCCGCCAGTACTGTGACTTCCAAAGCCAGAGCCACATGTGC 644
 OY 183 TGATTTTAAATAGTAAATCATCATCTGCTTACGGGTGGGGGTGGGGTACGCTTAG 242
 DB 645 TCATCAAACTTGCAATTAACACAGTTGGCGGAGATGGCTGTGGAGCTGGGCTTAACTGA 704
 OY 243 TAGTCAGTGGGAGCAACACTTATTTGTTAGCTATTTCTGTCTTAATAGTGTCACT 302
 DB 705 TGGTCTCTTTTGTCTCCCTTCTTGTGAGGTAAGCTACTGTCTTCTTAAGAGTATTT 764
 OY 303 ATTACAA 309
 DB 765 ATGCCAA 771

RESULT 11
 AAC77977

ID. AAC77977 standard; cDNA: 4040 BP.

AC AAC77977;

DT 08-FEB-2001 (first entry)

DE Human cancer associated gene sequence SEQ ID NO:371.

XX Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
 KW antidiabetic; antileukemic; antirheumatic; antibacterial; antiviral;
 KW antiinflammatory; antihypertoid; antiallergic; thrombotic; cardiac;
 KW dermatologic; neuroprotective; thrombolytic; coagulant; noctropic;
 KW vasotropic; antiproliferative; angiogenic; gene therapy; inflammation;
 KW immune disorder; hematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW hemostatic; thrombolytic; cardiovascular disorder; infection; ss.
 KW neurological disease; drug screening; ss.

XX Homo sapiens.

OS WO200055350-A1.

PN 21-SEP-2000.

DE 08-MAR-2000; 2000MO-US05882.

PR 12-MAR-1999; 99US-0124270.

XX (HUMAN-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

DR P-PSDB; AAB43768.

XX Novel isolated nucleic acids comprising sequences encoding peptides

PT useful for treating or diagnosing e.g. cancer -
 PS Claim 1; Page 918-920; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given
 XX in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antileukemic; antirheumatic; antibacterial; antiviral;
 CC antiinflammatory; antihypertoid; antiallergic; thrombotic; cardiac;
 CC dermatologic; neuroprotective; thrombolytic; coagulant;
 CC vasotropic; antiproliferative; angiogenic; gene therapy; inflammation;
 CC immune disorder; hematopoietic cell disorder; autoimmune disorder;
 CC allergic reaction; graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC the present invention.

SO Sequence 4040 BP; 1173 A; 789 C; 790 G; 1281 T; 7 other;

Query Match 10.3%; Score 36.6; DB 21; Length 4040;
 Best Local Similarity 49.7%; Pred. No. 0.59;

Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 123 TGTATGCGAGTCCCAACATTTCTACGGTGTATATATAGACGGTACAGATCAGC 182
 DB 586 TGACCCCTGGCAGCAACCCGCCAGTACTGTGACTTCCAAAGCCAGAGCCACATGTGC 645
 OY 183 TGATTTTAAATAGTAAATCATCATCTGCTTACGGGTGGGGGTGGGGTACGCTTAG 242
 DB 646 TCATCAAACTTGCAATTAACACAGTTGGCGGAGATGGCTGTGGAGCTGGGCTTAACTGA 705
 OY 243 TAGTCAGTGGGAGCAACACTTATTTGTTAGCTATTTCTGTCTTAATAGTGTCACT 302
 DB 706 TGGTCTCTTTTGTCTCCCTTCTTGTGAGGTAAGCTACTGTCTTCTTAAGAGTATTT 765
 OY 303 ATTACAA 309
 DB 766 ATGCCAA 772

RESULT 12

ID. ABL61761 standard; DNA: 5544 BP.

AC ABL61761;

DT 15-MAY-2002 (first entry)

DE Colon adenocarcinoma related gene sequence SEQ ID NO:98.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 KW gene; ds.

XX Homo sapiens.

OS WO200194629-A2.

PN 13-DEC-2001.

DE 30-MAY-2001; 2001MO-US10838.

PR 05-JUN-2000; 2000US-209473P.

XX
PS Claim 1; SEQ ID No 165; 24bp; English.

CC The invention relates to a nucleic acid comprising a sequence at
CC least 18 bases in length of a segment of the chemically pretreated DNA
CC of genes associated with pharmacogenomics according to one of the
CC sequences of the genes ADRH6 (NM_000693), CYP11A (NM_000781), CYP11B1
CC (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
CC (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC MRP (NM_004996, NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC NM_019899) and their complementary sequences, or a sequence (S1) chosen
CC from 87 sequences and their complements. The chemical pretreatment
CC is bisulphite treatment to convert cytosines (but not methyl-cytosines)
CC into uracils. Also included are an oligomer (II) in particular an
CC oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC each case at least one base sequence having a length of 9 nucleotides
CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in
CC an array for analysing diseases associated with the methylation state
CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC of the 87 sequences. The oligomers may also be used as PCR primers.
CC The set of 87 nucleic acids and their complements is useful for diagnosis
CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC .ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 1668 BP; 480 A; 15 C; 359 G; 814 T; 0 other;

Query Match 10.0%; Score 35.6; DB 24; Length 1668;

Best Local Similarity 51.2%; Pred. No. 0.84; Mismatches 79; Indels 0; Gaps 0;

Matches 83; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 141 ATTTCTAAGCGGTATATATAGACAGCGTACAGATCAGCTGATTTATATAGTAA 200
DB 387 ATTTTATATCTGGGTATATATAGTAACTTTTCTGTAGTTTATTTATTTGTA 446
QY 201 TCATCGTCTTACGGGGTGGGTGGTGGGGTACGTTAGTAGTCGACTGGGCACA 260
DB 447 ATATTAGTGAAGTATTTGGGGTTTGTGGATGGTGAATGATTTGGGAAGGGTTG 506
QY 261 ACTTATGTGTAGTATTTCTGTGTTAATGATGCACT 302
DB 507 GTTTTGGGGATTTTATTTATTTGTTTAAATGAAGT 548

Search completed: March 12, 2003, 08:23:48
Job time : 566 secs

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 10:26:12 ; Search time 53.5 Seconds

(without alignments)
2046.423 Million cell updates/sec

Title: US-09-936-011-3

Perfect score: 357
Sequence: 1 atgctaggggaataaccgc.....gtatgctgcttggttaa 357

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.4	8.5	9595	3	US-09-014-416-4
2	29.6	8.3	2087	4	US-09-097-199-83
3	29.6	8.3	2505	4	US-09-097-199-85
4	29.6	8.3	4285	4	US-09-410-464-1
5	29	8.1	1370	4	US-09-026-408-12
6	29	8.1	1371	4	US-09-026-408-1
7	28.8	8.1	5163	3	US-08-700-651-1
8	28.8	8.1	5163	3	US-08-928-361B-4
9	28.8	8.1	5318	3	US-08-700-651-2
10	28.8	8.1	5318	3	US-08-928-361B-3
11	28.8	8.1	5883	3	US-08-404-445-1
12	28.8	8.1	6060	5	PCT-US96-09430-7
13	28.8	8.1	8442	4	US-09-272-032-6
14	28.6	8.0	1506	2	US-08-663-566A-8
15	28.6	8.0	1506	2	US-08-023-610-8
16	28.6	8.0	1506	2	US-08-288-065A-8
17	28.6	8.0	1506	2	US-08-362-240A-8
18	28.6	8.0	1506	2	US-08-804-372A-6
19	28.6	8.0	1506	5	PCT-US95-10245-8
20	28.4	8.0	3454	4	US-09-549-804C-1
21	28.4	8.0	3454	4	US-08-961-527-207
22	28.4	8.0	5173	4	US-08-801-308-2
23	28.4	8.0	16569	4	US-09-097-889-2
24	28.4	8.0	16569	4	US-09-377-856-1
25	28.4	8.0	16569	4	US-09-302-681-2
26	28.4	8.0	18596	4	US-09-318-448-11
27	28.2	7.9	1170	5	PCT-US96-05320A-900

C 28	28.2	7.9	1316	3	US-08-460-576-1	Sequence 1, Appl
C 29	28.2	7.9	5311	3	US-08-928-361B-2	Sequence 2, Appl
C 30	28.2	7.9	7334	3	US-08-928-361B-1	Sequence 1, Appl
C 31	28	7.8	549	1	US-08-196-945-1	Sequence 1, Appl
C 32	28	7.8	7766	4	US-09-125-619-3	Sequence 3, Appl
C 33	27.8	7.8	3134	2	US-08-533-669A-1	Sequence 1, Appl
C 34	27.8	7.8	3134	4	US-09-183-861-1	Sequence 1, Appl
C 35	27.8	7.8	3134	4	US-09-022-765-1	Sequence 1, Appl
C 36	27.6	7.7	1251	2	US-08-655-704B-16	Sequence 16, Appl
C 37	27.6	7.7	1251	3	US-09-107-755-16	Sequence 16, Appl
C 38	27.6	7.7	2265	3	US-09-369-618-3	Sequence 3, Appl
C 39	27.6	7.7	2265	3	US-08-332-766A-1	Sequence 3, Appl
C 40	27.4	7.7	377	2	US-08-196-446B-3	Sequence 3, Appl
C 41	27.4	7.7	1022	1	US-08-870-693-3	Sequence 3, Appl
C 42	27.4	7.7	1022	2	US-09-484-970B-138	Sequence 138, App
C 43	27.4	7.7	3054	4	US-09-008-172-1	Sequence 1, Appl
C 44	27.4	7.7	4310	3	US-09-210-361-5	Sequence 5, Appl
C 45	27.4	7.7	4310	4		

ALIGNMENTS

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RESULT 1
US-09-014-416-4
; Sequence 4, Application US/09014416
; Patent No. 6153421
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Bukh, Jens
; APPLICANT: Emerson, Susanne U.
; APPLICANT: Purcell, Robert H.
; TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 20264276
; CURRENT APPLICATION NUMBER: US/09/014,416
; CURRENT FILING DATE: 1998-01-27
; EARLIER APPLICATION NUMBER: US 60/053,062
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9595
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-4

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Best Local Similarity 61.2%; Pred. No. 6.1;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGCTGTGGGAATTAACCGCTCGACCCATTAAGATGCTATTGTTGGTGTGTTGT 60
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Db 9371 ATGAACGGGAGGAGTACCACTCAAGCCATTTCGTTTATTTTATTTT 9430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GTTGTGCTTCTTCTTGTATT 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9431 TTTTATTTTCTTTTATTTT 9450
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RESULT 2
US-09-097-199-83/C
; Sequence 83, Application US/09097199
; Patent No. 6218529
; GENERAL INFORMATION:
; APPLICANT: An, Gang
; APPLICANT: O'Hara, S. Mark
; APPLICANT: Ralph, David
; APPLICANT: Veltl, Robert
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
; PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
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US-09-026-408-12

US-09-026-408-1

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Best Local Similarity	54.1%	Pred. No.	6.9				
Matches	59	Conservative	0	Mismatches	50	Indels	0
						Gaps	0

Page 7

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? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212)977-9550
? TELEFAX: (212)664-0525
? TELEX: 422523
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1506 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1506
? US-08-023-610-8

Query Match 8.0%, Score 28.6; DB 2; Length 1506;
Best Local Similarity 61.3%; Pred. No. 9.7;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0

QY 190 AATATACAATCATCGTCGTTACGGGTCGGGTCTGGGGGAGACGTTAGTACTGCA 249
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DB 1383 AAGAGCAACACCCATGCTATTATACGTTACGGCAGCTTTGGGATGGCTGTAAATTTTACG 1442

QY 250 GTTGGGAGCAACTT 264
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DB 1443 GATGGGATATCAT 1457

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Job time : 75.5 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 13:59:58 ; Search time 743 Seconds
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320.925 Million cell updates/sec

Title: US-09-936-011-3
Perfect score: 357
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 478924 seqs, 33395956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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- 10: /cgn2_6/ptodata/2/pubna/US09_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.6	10.3	4039	10 US-09-925-301-371	Sequence 371, App
2	34.2	9.6	493	10 US-09-864-761-5863	Sequence 5863, Ap
3	32.8	9.2	2361	10 US-09-815-242-8565	Sequence 8565, Ap
4	32.2	9.0	234	10 US-09-864-761-2826	Sequence 2826, A
5	31.6	8.9	155074	9 US-10-026-188-6	Sequence 6, Appl1
6	31.2	8.7	472	10 US-09-864-761-11710	Sequence 11710, A
7	30.8	8.6	276	10 US-09-864-761-25120	Sequence 25120, A
8	30.8	8.6	537	10 US-09-864-761-8390	Sequence 8390, Ap
9	30.4	8.5	867	10 US-09-737-178-97	Sequence 97, Appl
10	30.4	8.5	967	10 US-09-983-531A-9	Sequence 9, Appl1
11	30.4	8.5	1333	10 US-09-737-178-130	Sequence 130, Appl
12	30.4	8.5	1668	10 US-09-792-2008-3	Sequence 3, Appl1
13	30.4	8.5	127197	9 US-09-754-853A-1	Sequence 1, Appl1
14	30.2	8.5	574	10 US-09-864-761-228	Sequence 228, App
15	30.2	8.5	669	10 US-09-864-761-17051	Sequence 17051, A
16	30.2	8.5	759	10 US-09-864-761-3336	Sequence 3336, Appl
17	30	8.4	401	10 US-09-864-761-3936	Sequence 3936, App
18	30	8.4	446	10 US-09-864-761-20659	Sequence 20659, A
19	29.6	8.3	287	9 US-09-535-459-1849	Sequence 1849, App

C 20	29.6	8.3	2960	9 US-10-098-841-16	Sequence 16, Appl
C 21	29.6	8.3	3098	9 US-10-098-841-15	Sequence 15, Appl
C 22	29.6	8.3	4285	9 US-10-104-580-1	Sequence 1, Appl1
C 23	29.6	8.3	9567	12 US-10-016-768-12	Sequence 12, Appl1
C 24	29.6	8.3	9574	12 US-10-016-768-9	Sequence 9, Appl1
C 25	29.4	8.2	594	10 US-09-864-761-7908	Sequence 7908, Ap
C 26	29.4	8.2	730	10 US-09-764-864-248	Sequence 248, App
C 27	29.4	8.2	753	10 US-09-764-853-177	Sequence 177, App
C 28	29.4	8.2	818	10 US-09-764-864-676	Sequence 676, App
C 29	29.4	8.2	873	10 US-09-764-853-178	Sequence 178, App
C 30	29.4	8.2	1030	10 US-09-878-574-4306	Sequence 4306, App
C 31	29.4	8.2	2901	10 US-09-801-368-371	Sequence 371, App
C 32	29.4	8.2	2934	9 US-09-938-901-7	Sequence 7, Appl1
C 33	29.4	8.2	10236	10 US-09-764-853-3185	Sequence 878, App
C 34	29.2	8.2	456	10 US-09-864-761-5185	Sequence 1585, App
C 35	29.2	8.2	474	10 US-09-864-761-1364	Sequence 1364, App
C 36	29.2	8.2	887	10 US-09-864-761-21484	Sequence 21484, A
C 37	29.2	8.2	1075	10 US-09-864-761-19241	Sequence 19241, A
C 38	29.2	8.2	1249	10 US-09-881-752A-223	Sequence 223, App
C 39	29.2	8.2	1403	10 US-09-864-761-2513	Sequence 2513, App
C 40	29.2	8.2	1635	10 US-09-864-761-20241	Sequence 20241, A
C 41	29.2	8.2	1973	10 US-09-864-761-4371	Sequence 3471, App
C 42	29.2	8.2	1981	10 US-09-864-761-4745	Sequence 4745, App
C 43	29	8.1	370	10 US-09-770-791-356	Sequence 356, App
C 44	29	8.1	479	10 US-09-864-761-768	Sequence 768, App
C 45	29	8.1	496	9 US-10-040-739-276	Sequence 276, App

ALIGNMENTS

RESULT 1
US-09-925-301-371
Sequence 371, Application US/09925301
Patent No. US2002052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OR INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 371
LENGTH: 4039
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
LOCATION: (1085)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-371

Query Match 10.38; Score 36.6; DB 10; Length 4039;
Best Local Similarity 49.7%; Pred. No. 0.25;
Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY	123	TGATTACGAGTCCCACTTTCTAAGCGGTGTATATAGACGATACAGATCAGC	182
DB	586	TGACCCCTGGCACCACACCCGACAGTGTGCTTCAAAAGCCACACATGTCC	645
QY	183	TGATTATATAGTAACATCATCGTGTACGGGTGGGTGGGTAGCGTTAG	242
DB	646	TGATCAACACTGCTTAAAGCAGTTGGGGGAGAGGCGTGGAGCTGGGGTTAAGTGA	705
QY	243	TATGCGAGTTGGGACGACACTTATTTGTTAGCTATTTCTTGTGTTAATAGTTCAC	302
DB	706	TGTTCTCTTTGCTCCCTTCTTGTGAGAGGTAAAGCTACTGCTTCTTAAAGGTATATT	765


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Sequence 11710, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
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PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 11710
LENGTH: 472
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004547.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.75
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86
US-09-864-761-11710

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Query Match	8.7%;	Score 31.2;	DB 10;	length 472;
Similarity	47.1%;	Pred. No. 4.4;		
Best Local	96;	Mismatches 108;	Indels 0;	Gaps 0;
Matches				

QY	36	TGACCATTGTTTGGTGTGTTTGTTGGCTTTCTTGTAATGCTGGCGTTCATGCA	95
	470	TGTACTTAATTAGACAGGTGCTGTGTACATGACACAACTTTGGCATATGATGATGATGGA	411
Db			
96	GCAAGCAGCTCCGACACATTTCTGGGGGTGATTTACGGAGTCCCAACATTTCTAAACGTGG	155	
YY			

Db	410	GAAGATGATCATCTGCTGATAGTATAGTACGAAATATAGTATAGTGGTGGTATGGTAG	351
QY	156	TATATATAGACCGGTACAGATAGCTGATTTTAAATAGTACAAATATCGTGGTTACGG	215
Db	350	TAGTATGATATACCATGGTGGTGTATGATGATATTTGATGATGTCACAGTATATAGTGGTGG	291
QY	216	GTCGGGTGGCTCTGGGGTAGCGT	239
Db	290	TAGTGGTATGATGGTATGGTGT	267

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Qy      216 GTCCGGTGGCTCTGGGGGTAGCGT 239
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Db      290 TAGTGTGATGATGGTGTGATGGTGT 267

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RESULT 7
US-09-864-761-25120/c

```
; APPLICANT: Penn. Sharron G.
```

```
;; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
```

FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864

;; PRIOR APPLICATION NUMBER: US 60/180,311
;; PRIOR FILING DATE: 2000-02-04
;; PRIORITY DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 09/632,360
PRIOR FILING DATE: 2000-08-03

; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,355
 ; PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006

; PRIOR APPLICATION NUMBER: FC1/0501/000
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: DCM/MS01/000

;; PRIOR APPLICATION NUMBER: PCT/US01/006
;; PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/000
PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/000

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,611

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PRIOR APPLICATION NUMBER: US 09/608,4
;
PRIOR FILING DATE: 2000-06-30
;

NUMBER OF SEQ ID NOS: 49117

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; LENGTH: 276
; TYPE: DNA

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OTHER INFORMATION: MAP TO AC012153.1
OTHER INFORMATION: EXPRESSED IN HEPA

OTHER INFORMATION: EXPRESSED IN BRAIN

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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25120
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ORGANISM: *Homo sapiens*
FEATURE:

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; OTHER INFORMATION: MAP TO AC012153.10 SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION:

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RESULT 9
US-09-737-178-97
: Sequence 97, Application US/09737178
: Patent No. US20010028295A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 867
TYPE: DNA
ORGANISM: Babesia microti
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(867)
OTHER INFORMATION: n=A,T,C or G
US-09-737-178-97

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Db 731 GTGCTGCTGGAAGATCTGTAGAACTTCAGTGTGTAGATCTCTCTGTGATTATG 790
Qy 203 ATCTGCT 210
Db 791 ACTGTGAT 798

RESULT 13
US-09-754-853A-1/C
Sequence 1, Application US/09754853A
Publication No. US2003000491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1
LENGTH: 127197
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 515002_region_G2
US-09-754-853A-1

Query Match
Best Local Similarity 59.1%; Score 30.4; DB 9; Length 127197;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 5 CTGAGGAATACCGCTGCAACCAATAGATGCTATTGCTGCTGCTGCTG 64
Db 24247 CTATTGAAATATATCTCGATTATGTAAGATCAGCTTTGTTCTGGAGACACTGTTG 24188
Qy 65 TGGCTTTCTTGTATGCTGGCGCTTCA 92
Db 24187 TTACTGCTCTGATGATATATCTTCTAT 24160

RESULT 14
US-09-864-761-228/C
Sequence 228, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 228
LENGTH: 574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL079301.14
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7
US-09-864-761-228

Query Match
Best Local Similarity 55.1%; Score 30.2; DB 10; Length 574;
Matches 59; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 147 TAACGGTGTATATATAGACGCGTACAGATCAGCTGATTTTATATACATCATCG 206
Db 367 TGAGGATGGTTGTCATAGATGATGATATGATGATCATGTTGATGTGTTGTTG 308
Qy 207 TGCTTACGGGTGGCGGTGGCTGGGCTTACGCTTACGATGCGAGTTG 253
Db 307 TGCTGATGGATGATGCTGCTGCTGCTGCTGATGATGTTGATGATG 261

RESULT 15
US-09-864-761-17051/C
Sequence 17051, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17051
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL079301.14
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7
; OTHER INFORMATION: EST HUMAN HIT: BE011604.1, EVALUATE 1.10e-01
; OTHER INFORMATION: NT HIT: g19628932, EVALUATE 1.10e-01
; US-09-864-761-17051

Query Match      8.5%; Score 30.2; DB 10; Length 669;
Best Local Similarity 55.1%; Pred. No. 11;
Matches 59; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 147 TAACGGTGTATATATAGACGCGTACAGATCAGCTGATTTTAAATAGTACATCATCG 206
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 TGAAGGATGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242

QY 207 TGGTTACGGGCGTGGTGGTGGGAGTAGCGTTAGTAGTACGAGTTG 253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 TGGTTACGGGCGTGGTGGTGGGAGTAGCGTTAGTAGTACGAGTTG 195
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Search completed: March 12, 2003, 08:12:50
Job time : 847 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2003, 06:32:01 ; Search time 1191.5 Seconds
(Without alignments)
4852.529 Million cell updates/sec

Title: US-09-936-011-3
Perfect score: 357
Sequence: 1 atgctaggaataaacgcgc.....gtaatggtcgtctgtgtaaa 357

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43.8	12.3	1101	17	CNS00LT2
2	42.8	12.0	1080	17	CNS00LEP
3	40.6	11.4	902	17	CNS006OP
4	39.2	11.0	598	13	BJ032222
5	38.4	10.8	1101	17	CNS00FOO
6	37.8	10.6	884	17	CNS00600

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	CNS00LT2	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			
2	CNS00LEP	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			
3	CNS006OP	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			
4	BJ032222	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			
5	CNS00FOO	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			
6	CNS00600	Drosophila melanogaster genome survey sequence TERT3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	1101 bp	DNA	GSS	1101 bp	DNA	GSS	14-JUN-1999			

ALIGNMENTS

AL098379 Drosophila
BB671302 BB671302
BF417205 UI-R-CNO-
BQ215809 AGENCOURT
AA134045 zoi17d11.f
AL066784 Drosophila
BB224881 BB224881
AO927406 RPCI-23-2
AL059400 Drosophila
AL106109 Drosophila
BM605179 17006870
AO23013 HS-5230.A
AL23200 Tetradon
BF678875 60215190
AL106871 Drosophila
AL068607 Drosophila
A2627893 1M0469118
BQ353390 PM1-HFO45
BG776437 602665521
BJ336822 BJ336822
BJ137716 BJ137716
AT501178 UI-R-C2P-
AV417568 AV417568
AV413481 AV413481
BF418198 UI-R-CNO-
AW524847 UI-R-BOO-
AA900710 UI-R-BO-
AA423714 AV423714
AV408287 AV408287
AV428494 AV428494
AV408779 AV408779
AV412428 AV412428
AT705708 UI-R-AD1-
BF417072 UI-R-CNO-
BE109288 UI-R-BJ1-
AL092839 Aradidops
A2276668 RPCI-23-1
BM385308 UI-R-ERI-
BM391584 UI-R-DYO-

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		/clone="BACR14J09"	
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Best Local Similarity 22.4% Pred. No. 4;			
Matches 57; Conservative 93; Mismatches 105; Indels 0; Gaps 0			
OY	36 TGTGCTATTGTTGTTGGTGTGTGTGCTTCTTTGATATTCGTGCGCTTCATGCA 95		
Db	524 TTKKTKKKKKTK 583		
OY	96 GCAACAGCTGCGACACATTCGTGGGCGTATAGCGAGTCCCAACTTTTCTACGCTGG 155		
Db	584 TBGGGCGKGBGGGGGCGKGGGGGCTTKKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 643		
OY	156 TATATATAGAGACGCTACAGATCAGCTGATTTTATAGTAAACAATCATCGCTTACGG 215		
Db	644 KKGTTKTKTKGBKTK 703		
OY	216 GTGCGGTGCGTGTGGGCGTACGCTAGTACGAGTGGCGACACTTATGCTTTAGC 275		
Db	704 KTKBKKKKKKKKBGGGKGGKGTBKTKTKTKTKTKTKTKTKTKTKTKTKTKTKTK 763		
OY	276 TATGTGTTCTGTGT 290		
Db	764 BCTTBVBTTKTKTKTK 778		
RESULT 4			
BJ032222			
LOCUS			
DEFINITION BJ032222 NIBB Mochil normalized Xenopus neurolia library Xenopus			
laevis cDNA clone Xl016a10 5', mRNA sequence.			
ACCESSION BJ032222			
VERSION BJ032222.1 GI:17378218			
KEYWORDS EST.			
SOURCE			
ORGANISM			
Xenopus laevis			
African clawed frog.			
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
Xenopodinae; Xenopus.			
1 (bases 1 to 598)			
Kikuyama,A., Terasaka,C., Mochil,M., Ueno,N., Shin-I,T. and Kohara			
,Y.			
TITLE			
JOURNAL			
COMMENT			
Expressed genes in X. laevis embryo			
Unpublished (2001)			
Contact: Tadasu Shin-I			
Center For Genetic Resource Information			
National Institute of Genetics			
1111 Yata, Mishima, Shizuoka 411-8540, Japan			
Tel: 81-559-81-6856			
Fax: 81-559-81-6855			
Email: tshin@genes.nig.ac.jp.			
FEATURES			
source			
1. 598			
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/db_xref="taxon:8355"			
/clone="Xl016a10"			
/clone_1lb="NIBB Mochil normalized Xenopus neurolia			
library"			
/tissue_type="whole embryo"			
/dev_stage="stage 15"			
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs			
were oligo-dT primed and directionally cloned. Staging			
according to Nieuwkoop and Faber. library is subtracted			
and was constructed by N. Garrett and A.M. Zorn,			

BASE COUNT	138 a	130 c	165 g	165 t
ORIGIN				
Query Match	11.0%;	Score 39.2;	DB 13;	Length 598;
Best Local Similarity	58.6%;	Pred. No. 8.6;		
Matches	68;	Conservative	0;	Mismatches 48; Indels 0; Gaps 0;
QY	36	TGCGCCATTGTTGTTGGTGTTCGTTGTCGCTTTCTTTGATATTCGTGGCGTTATGCA	95	
DB	249	TGCGCTGCAGCGCTGTGGTTGTTCTGTTCGTGGGACAGGCTTGTATTAATCTTGGCGACGACCT	308	
QY	96	GCAAGCAGCTGCAGACATCTTGGGGGTATTACGAGATCCCAACATTTTCTAACG	151	
DB	309	ACTACACAGCTGTGGGCTTCACTGAGAGATCCCTACTGCTTGGCACACTAATCAGC	364	
RESULT 5				
CNS00FOO				
LOCUS				
DEFINITION	CNS00FOO	1101 bp	DNA	linear
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC:			
VERSION	BAC314F03 of RPCT-98 library from Drosophila melanogaster (fruit			
KEYWORDS	fly), genomic survey sequence.			
SOURCE	AL070854			
ORGANISM	AL070854.1	GI:4950896		
REFERENCE	Drosophila melanogaster.			
AUTHORS	Drosophila melanogaster			
TITLE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotet;			
JOURNAL	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
COMMENT	Ephydroidea; Drosophilidae; Drosophila.			
	1 (bases 1 to 1101)			
	Genoscope.			
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequenage			
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr			
	- Web : www.genoscope.cns.fr)			
	Determination of this BAC-end sequence was carried out as part of a			
	collaboration with the Berkeley Drosophila Genome project (BDGP).			
	The BDGP is constructing a physical map of the Drosophila			
	melanogaster genome using these BACs. For further information			
	please see http://www.fruitfly.org The BDGP Drosophila			
	melanogaster BAC library was prepared by Kazutoyo Oseegawa and			
	Aaron Mamoser in Pieter de Jong's laboratory in the Department of			
	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,			
	NY. The library is named RPCT-98 and was constructed by partial			
	ECORI digestion of Drosophila DNA provided by the BDGP from the			
	isogenic strain Y2; cn bw sp, the same strain used for the BDGP's			
	P1 and EST libraries. A more detailed description of the library			
	and how to order individual BAC clones, the entire library, or			
	filters for hybridization from the BACPAC Resource Center can be			
	found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .			
FEATURES				
source	Location/Qualifiers			
	1..1101			
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	/clone_lib="RPCT-98"			
	/note="end : T7"			
BASE COUNT	167 a	84 c	86 g	155 t
ORIGIN				
Query Match	10.8%;	Score 38.4;	DB 17;	Length 1101;
Best Local Similarity	14.6%;	Pred. No. 15;		
Matches	43;	Conservative	129;	Mismatches 122; Indels 0; Gaps 0;
QY	22	CGACCCATTAAGATGTCCTATTGTTGGTGTGTTGCTGTGCTTCTTTGATATG	81	
DB	804	MGGMMMGAMMTGKGGKGTGTGVBGCTGKXKKNKGTAKKMMGKWKMDMNTKTKTKTK	863	
QY	82	CTGGCGTTTCAGCAAGCAAGCAGCTGCACACATTCCTGCGGGGTGATTACGAGTCCCAACA	141	
DB	864	TKTKTATTTATTKTKTKKKKKKKKKTKTAKKKKKAKAKAKKMMGDDGAKKATPAAMAA	923	

[illegible][illegible]


```

FEATURES
source
location/Qualifiers
1..328
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530088K07"
/clone_lib="RIKEN full-length enriched, adult male aorta
and vein"
/sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was

```


P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 939
location/Qualifiers

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACR26H16"

/clone_lib="RPCI-98"

/note="end : TET3"

BASE COUNT 71 a 349 c 104 g 180 t 235 others

ORIGIN

Query Match 10.0%; Score 35.8; DB 17; Length 939;

Best Local Similarity 11.3%; Pred. No. 67;

Matches 26; Conservative 115; Mismatches 90; Indels 0; Gaps 0;

```
OY 12 AATAACCGCTGACCAATAGAAATGTCCTATTTGTTGGTGTGTTGGCTTT 71
   || || || || || || || || || || || || || || || || || ||
Db 603 AAGAAGGCGAGGCGACGAGAGAGAGACGAKAKKKKKKKKKKKKKKKKK 544
OY 72 CTTGTATTGCTGGGCGTCATGCACAGCAGCTCGACACATCTCGGGGTGATTACGG 131
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 KDKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 484
OY 132 AGTCCCAACATTTCTAAGCGGTGTATATATAGAGCGGTACAGATCATTTTAA 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 483 AKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 424
OY 192 TAGTAACAATCATCGTCTTAAGGCGTGGGTGCTGGGGGTAGCGTTAG 242
   : : | : | : | : | : | : | : | : | : | : | : | : |
Db 423 AKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 373
```

Search completed: March 12, 2003, 10:11:21
Job time : 1196.5 secs

